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<110> MURDIN, Andrew D.; OOMEN, Raymond P; and WANG, Joe
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4/83

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5/83

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7/83

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9/83

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10/83

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50	gat tta gtg act gct aac gtt ctt gta gcg atg cag atg atg atg tta	739
	Asp Leu Val Thr Ala Asn Val Leu Val Ala Met Gln Met Met Met Leu	
	200 205 210	
	tcc cct cta tcg att tcg tta cct tta aag tta ctt ttg atc gtc atg	787
	Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu Leu Ile Val Met	
	215 220 225	
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	Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu Met Ile Ser Phe Lys	
	230 235 240 245	

11/83

taaggacacg tgccgtgtta gcattttcg caactagtt caaatctgtt cttttgagt 895
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 Met Lys Phe Phe Ser
 1 5

tta att ttt aaa gat gat gat gtc tcc cca aat aag aag gtt tta tct 163
 Leu Ile Phe Lys Asp Asp Asp Val Ser Pro Asn Lys Lys Val Leu Ser
 40 10 15 20

cct gaa gct ttc tct gct ttc ctt gat gcc aaa gag ctg tta gaa aaa 211
 Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys Glu Leu Leu Glu Lys
 25 30 35

aca aaa gcc gat agc gaa gcc tat gtt gca gag aca gaa caa aag tgt 259
 Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu Thr Glu Gln Lys Cys
 40 45 50

50 gca caa att cgt caa gaa gct aaa gat caa gga ttt aaa gag gga tct 307
 Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly Phe Lys Glu Gly Ser
 55 60 65

gaa tcc tgg agc aag caa att gct ttc tta gaa gaa gaa act aaa aat 355
 Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu Glu Thr Lys Asn
 70 75 80 85

cta cgc ata aga gta cgc gag gcc ttg gtt cct ctg gca att gcg agt 403
 Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro Leu Ala Ile Ala Ser
 60 90 95 100

12/83

	gtg agg aaa atc att ggg aag gaa ctc gaa tta cat cct gaa act att	451
	Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu His Pro Glu Thr Ile	
	105 110 115	
	gtc tct att att tct caa gca ttg aaa gag ctc aca caa aat aaa cat	499
	Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu Thr Gln Asn Lys His	
	120 125 130	
10	atc att atc tct gtc aat ccc aaa gat tta cct ctt gtt gag aaa agt	547
	Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro Leu Val Glu Lys Ser	
	135 140 145	
	cgt cct gaa ctc aag aac atc gtg gag tat gct gac tcc tta att ctt	595
	Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala Asp Ser Leu Ile Leu	
	150 155 160 165	
20	aca gca aaa cct gat gtt act cct ggg ggt tgc att atc gag act gaa	643
	Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys Ile Ile Glu Thr Glu	
	170 175 180	
	gca ggg atc atc aat gcg cag ctt gat gta caa tta gat gcc tta gaa	691
	Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln Leu Asp Ala Leu Glu	
	185 190 195	
	aaa gct ttc tcg act ata cta aaa gcg aag aac cct gta gac gag cca	739
	Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn Pro Val Asp Glu Pro	
	200 205 210	
30	tct gag act tca tca tcc acg gat tct tct tct tta tct aat gat cag	787
	Ser Glu Thr Ser Ser Thr Asp Ser Ser Ser Leu Ser Asn Asp Gln	
	215 220 225	
	gat aag aaa gaa taaaggatt cactattatg cgatccattt ttcgattttc	839
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	tgt aca agc tgt aac agc agg tct cta att gtg cac ggt ctt cct ggc Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val His Gly Leu Pro Gly 10 15 20	163
20	aga gaa gcg aat gag att gtg gtg ctt ttg gta agc aaa ggg gtg gct Arg Glu Ala Asn Glu Ile Val Val Leu Leu Val Ser Lys Gly Val Ala 25 30 35	211
	gca caa aaa ttg cct caa gct gca gcg gct aca gcc gga gca gct act Ala Gln Lys Leu Pro Gln Ala Ala Ala Thr Ala Gly Ala Ala Thr 40 45 50	259
	gag caa atg tgg gat atc gcg gtt ccg tca gca caa atc aca gag gcc Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala Gln Ile Thr Glu Ala 55 60 65	307
30	ctt gcc att cta aat caa gcg ggt ctt cca cgt atg aaa ggg aca agc Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg Met Lys Gly Thr Ser 70 75 80 85	355
	ctg tta gat ctt ttt gca aaa caa ggt ctt gtt cct tcc gag ctt cag Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val Pro Ser Glu Leu Gln 90 95 100	403
40	gaa aaa atc cgt tat caa gaa ggc tta tca gaa cag atg gcc tct acg Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu Gln Met Ala Ser Thr 105 110 115	451
	att aga aaa atg gat ggc gtt gtc gat gcc tca gta cag att tcc ttc Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser Val Gln Ile Ser Phe 120 125 130	499
	act aca gaa aat gaa gat aat ctt cct tta aca gcc tct gtg tat att Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr Ala Ser Val Tyr Ile 135 140 145	547
50	aag cat cga ggg gtt ttg gac aat ccg aac agc att atg gtt tcc aaa Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser Ile Met Val Ser Lys 150 155 160 165	595
	att aag cgc ctt att gca agt gct gtt cca gga ctt gtg cca gag aac Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly Leu Val Pro Glu Asn 170 175 180	643
60	gtc tct gta gtg agc gat cgc gca gct tat agt gat att aca att aat Val Ser Val Val Ser Asp Arg Ala Ala Tyr Ser Asp Ile Thr Ile Asn 185 190 195	691

14/83

ggt cct tgg gga tta aca gaa gaa atc gat tat gtt tct gtt tgg ggt Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr Val Ser Val Trp Gly 200 205 210	739
att att ctt gcg aag tct tcg ctc acc aaa ttc cgt ctc att ttt tat Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe Arg Leu Ile Phe Tyr 215 220 225	787
10 gtc ttg att ctc att tta ttt gtt att tct tgt ggt ctc ctt tgg gtc Val Leu Ile Leu Ile Phe Val Ile Ser Cys Gly Leu Leu Trp Val 230 235 240 245	835
att tgg aaa act cat act ctc att atg act atg gga ggt aca aaa ggg Ile Trp Lys Thr His Thr Leu Ile Met Thr Met Gly Gly Thr Lys Gly 250 255 260	883
20 ttc ttc aac cct aca cca tat aca aag aat gcc ttg gaa gcc aag aaa Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala Leu Glu Ala Lys Lys 265 270 275	931
gcc gag gga gca gct gct gac aaa gag aaa aag gat gca gat tca Ala Glu Gly Ala Ala Asp Lys Glu Lys Lys Glu Asp Ala Asp Ser 280 285 290	979
cag ggg gaa agc aaa aat gcg gaa acc agt gat aaa gac tct agt gat Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp Lys Asp Ser Ser Asp 295 300 305	1027
30 aaa gat gct cca gaa gga agc aat gaa att gag ggt gct tagtgactgc Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu Gly Ala 310 315 320	1076
caacactttt ggaactctag acatcttgat gaagcactcc aaggaagatg acctctccag 1136 gtttcttctt aaaaatcttc ttgttgaatc tcctcatccc gaagaaaatcc cttaaaaatc 1196 ttta 1200	
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Met Thr Ile Arg Val
1 5

10 cga aac ctt gcc tac tct gta aat aag aaa aag att cta gat ggt gta 163
Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Ile Leu Asp Gly Val
10 15 20

act ttt tct tta gag cga ggg cac att aca ctg ttt gtt ggg aag agt 211
Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu Phe Val Gly Lys Ser
25 30 35

20 ggt tca gga aaa aca atg att tta cgt gct ttg gcg ggc tta gtc cag 259
Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu Ala Gly Leu Val Gln
40 45 50

ccc act caa gga gat att tgg att gaa ggg gag gct cca gct cta gtt 307
Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu Ala Pro Ala Leu Val
55 60 65

ttc caa caa ccc gag tta ttt tcc cat atg aca gta tta gga aat tgc 355
Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr Val Leu Gly Asn Cys
70 75 80 85

30 acc cat cca caa atc cat atc aag ggt cgt agt acc gaa gaa gct cga 403
Thr His Pro Gln Ile His Ile Lys Gly Arg Ser Thr Glu Glu Ala Arg
90 95 100

gaa aag gcg ttc gag ctt tta cat ttg ttg gat att gaa gag gtt gct 451
Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp Ile Glu Glu Val Ala
105 110 115

40 aag aat tat cct gac cag ctc tct ggg gga caa aaa caa cgt gtg gct 499
Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala
120 125 130

att gta cgt tct tta tgt atg gat aaa cat aca tta ctt ttt gat gaa 547
Ile Val Arg Ser Leu Cys Met Asp Lys His Thr Leu Leu Phe Asp Glu
135 140 145

cct aca tcg gct tta gat cct ttt gct acg gca tcg ttc cga cat ctt 595
Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala Ser Phe Arg His Leu
150 155 160 165

50 tta gaa aca ctt cga gac cag gaa ctg act gta ggg tta act act cat 643
Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val Gly Leu Thr His
170 175 180

gac atg caa ttt gtt cat agt tgt ttg gat cgt atc tat ctt ata gat 691
Asp Met Gln Phe Val His Ser Cys Leu Asp Arg Ile Tyr Leu Ile Asp
185 190 195

60 caa gga act gtt gcg ggg gtc tat gac aag cgt gac gga gag ctc gat 739
Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg Asp Gly Glu Leu Asp
200 205 210

tct ggt cat cca tta tcg aaa tat atc cac tct gct caa taggactaca Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser Ala Gln 215 220 225	788
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40	
ttt acc tat cta tgc atc atc ttc tac gga tct tgt gca tcg tta tct Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser Cys Ala Ser Leu Ser 10 15 20	163
tta cat gca gga ctc tct ttc cca gaa gta cgt gga gct acg gct gct Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg Gly Ala Thr Ala Ala 25 30 35	211
gtt gtc cat gcc gac tct ggg aag gta ttc tat gat aaa gac ata gat Val Val His Ala Asp Ser Gly Lys Val Phe Tyr Asp Lys Asp Ile Asp 40 45 50	259
gct gta atc tat cct gcc agc atg acg aaa atc gca act gcc ctc ttt Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile Ala Thr Ala Leu Phe 55 60 65	307
atc cta aag cac tat ccc aca gtc ctc gat act ctc atc aaa gtc aaa Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr Leu Ile Lys Val Lys 70 75 80 85	355
60	

17/83

	caa gat gcg atc gct tcc atc act ccg caa gca aaa aaa caa tca gga		403
	Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala Lys Lys Gln Ser Gly		
	90	95	100
	tat cgt agt cct ccc cac tgg tta gaa act gat gga tct aca ata cag		451
	Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp Gly Ser Thr Ile Gln		
	105	110	115
10	ctc cat ctt cga gaa gag ctt tta ggg tgg gac ctg ttc cac gcc tta		499
	Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp Leu Phe His Ala Leu		
	120	125	130
	ctg gtc tgt tct gct aat gat gct gcg aat gtc tta gct atg gca tgt		547
	Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val Leu Ala Met Ala Cys		
	135	140	145
20	tgc gga tct gta gag aag ttt atg gat aag ctg aac ttc ttc tta aaa		595
	Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu Asn Phe Phe Leu Lys		
	150	155	160
	165		
	gaa gaa atc ggc tgc act cat acc cat ttt aat aat ccc cat ggg tta		643
	Glu Glu Ile Gly Cys Thr His Thr His Phe Asn Asn Pro His Gly Leu		
	170	175	180
	cat cat ccg aat cac tat act aca acc cgt gat ctt att agc atc atg		691
	His His Pro Asn His Tyr Thr Thr Arg Asp Leu Ile Ser Ile Met		
	185	190	195
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	Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly Val Ile Ser Thr Thr		
	200	205	210
	agc tat aaa ata ggg gct aca aac ctg cat ggc gaa cgg atc cta tcc		787
	Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly Glu Arg Ile Leu Ser		
	215	220	225
40	cca aca aac aaa ttg ctt ctt cct ggg tct acc tac cac tat ccc cca		835
	Pro Thr Asn Lys Leu Leu Pro Gly Ser Thr Tyr His Tyr Pro Pro		
	230	235	240
	245		
	gct tta gga ggg aaa aca ggg acc acc aag act gca ggg aaa aat cta		883
	Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr Ala Gly Lys Asn Leu		
	250	255	260
	att atg gct gaa aaa aat aac cgc ctc ttg gta acg atc gca acg		931
	Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu Val Thr Ile Ala Thr		
	265	270	275
50	ggc tat tcg ggt cct gtg agt gat ctc tac caa gat gtc att gct cta		979
	Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln Asp Val Ile Ala Leu		
	280	285	290
	tgt gaa acg gta ttt aac gag ccg cta tta aga aaa gag ctc gtc ccc		1027
	Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg Lys Glu Leu Val Pro		
	295	300	305
60	ccc tcc gac tgt ctc caa tta gaa ata gcg aat ctt ggg aag ctt tct		1075
	Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn Leu Gly Lys Leu Ser		
	310	315	320
	325		

18/83

tgc cct ctt cct gag gga ctc tac tat gac ttc tat gcc tcc gaa gat Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe Tyr Ala Ser Glu Asp 330 335 340	1123
cgc gaa cct ctt tct gta tct ttt att gca cat gcg gac gcc ttc cct Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His Ala Asp Ala Phe Pro 345 350 355	1171
10 att gaa caa gga gat ctt ctt ggt cat tgg gtt ttt tat gac gat gaa Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val Phe Tyr Asp Asp Glu 360 365 370	1219
ggc aag aaa att tct tcc cag cct ttc tat gcc cct tgt cgt ttt gag Gly Lys Lys Ile Ser Ser Gln Pro Phe Tyr Ala Pro Cys Arg Phe Glu 375 380 385	1267
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tat aga acc tat atg tct ata acc atg ctg ctc atg tat ttt cgc atc Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu Met Tyr Phe Arg Ile 410 415 420	1363
cgc aag cac cgc aag tat aaa aat tta aaa cac tat tct aaa atc Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His Tyr Ser Lys Ile 425 430 435	1408
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19/83

	tcgcaataat aacctgccta aacgatcttg taaacgactt atg gct tct aat ccc Met Ala Ser Asn Pro 1	115
	att tta cag ata gag gat cta tcc ata acc ttg gca aaa caa cgc caa Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu Ala Lys Gln Arg Gln 10 15 20	163
10	cag tac ccc atc gtc caa tct tta tcg ttt act atc aat gaa gga caa Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr Ile Asn Glu Gly Gln 25 30 35	211
	acc tta gca atc att gga gaa tca gga tca gga aaa tct gtc tct gcg Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Val Ser Ala 40 45 50	259
20	cat gca atc ctt cga tta ctt cct tgc ccc cca ttt tct gtt tct ggc His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro Phe Ser Val Ser Gly 55 60 65	307
	cag gtc aac ttc caa ggc cac aac tta ctt acg gct tcg cgc tct ata Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr Ala Ser Arg Ser Ile 70 75 80 85	355
	caa aaa aag att ata ggg aca gaa att tct atg atc ttt caa aac ccg Gln Lys Ile Ile Gly Thr Glu Ile Ser Met Ile Phe Gln Asn Pro 90 95 100	403
30	caa gca tct cta aac ccc gtg ttt act att gaa cag cag ttt cga gaa Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu Gln Gln Phe Arg Glu 105 110 115	451
	att att cat acc cac cta gcc tta act gca gaa gtt gct aaa gaa aag Ile Ile His Thr His Leu Ala Leu Thr Ala Glu Val Ala Lys Glu Lys 120 125 130	499
40	atg tta tac gct ctt gaa gaa aca ggg ttt cat gat ccc agg ctg tgc Met Leu Tyr Ala Leu Glu Glu Thr Gly Phe His Asp Pro Arg Leu Cys 135 140 145	547
	ttg aat ctc tac ccc cac caa ctc tct gga ggg atg ctt caa aga att Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly Met Leu Gln Arg Ile 150 155 160 165	595
	tgc att gcc atg gcg ctc ctc tgt tct cct aaa ctt ctt att gct gat Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys Leu Leu Ile Ala Asp 170 175 180	643
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	tta cta aaa aca cta cag aaa aaa acg gga atg agc ctt ctt att att Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met Ser Leu Leu Ile Ile 200 205 210	739
60	acc cat aat atg gga gtc gtt gca gaa act gct gat gac gtg ctc gtg Thr His Asn Met Gly Val Val Ala Glu Thr Ala Asp Asp Val Leu Val 215 220 225	787

20/83

	ctc tat gca gga cgc atg gta gaa tgt gcc cct gcg gtt caa atg ttc	835
	Leu Tyr Ala Gly Arg Met Val Glu Cys Ala Pro Ala Val Gln Met Phe	
230	235	240
	245	
	cat aat cct tct cat ccc tat acc cga gat ctt tta gca tcc aga ccc	883
	His Asn Pro Ser His Pro Tyr Thr Arg Asp Leu Leu Ala Ser Arg Pro	
250	255	260
10	tct cta caa ccg caa caa cta ggt tcc ttc aac ccc att cca gga cag	931
	Ser Leu Gln Pro Gln Gln Leu Gly Ser Phe Asn Pro Ile Pro Gly Gln	
	265	270
	275	
	ccc cca cac tac acg gcc ttt ccc tcg gga tgt cgc tat cac cct aga	979
	Pro Pro His Tyr Thr Ala Phe Pro Ser Gly Cys Arg Tyr His Pro Arg	
280	285	290
20	tgc tca aaa att tta aat cga tgt tct gcg gaa gct cca gaa atc tat	1027
	Cys Ser Lys Ile Leu Asn Arg Cys Ser Ala Glu Ala Pro Glu Ile Tyr	
	295	300
	305	
	ccg gta cgc gaa ggt cac aaa gta agg gtt ggc tgt atg acg act aat	1075
	Pro Val Arg Glu Gly His Lys Val Arg Val Gly Cys Met Thr Thr Asn	
310	315	320
	325	
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	Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu Thr Lys His Tyr Tyr	
	330	335
	340	
30	aag cgt tcc ttt tgg ttt cag gga aag aca att gcc agt cgt cct gtt	1171
	Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile Ala Ser Arg Pro Val	
	345	350
	355	
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	360	365
	370	
40	gga gaa tct gga tca ggg aaa agt acc ctg gcg tta gct ctc gca ggt	1267
	Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala Leu Ala Leu Ala Gly	
	375	380
	385	
	ctc cta cct ctc acc tct ggg ttc tta act ttt aac ggc acc cca atc	1315
	Ieu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe Asn Gly Thr Pro Ile	
	390	395
	400	405
	aag ttg cat tct aaa cac gga cgc cat caa tta cga tct caa gta cgg	1363
	Lys Leu His Ser Lys His Gly Arg His Gln Leu Arg Ser Gln Val Arg	
	410	415
	420	
50	ttg gtc ttt caa aat cca caa gct tca tta aac ccg cga aaa act atc	1411
	Ieu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Arg Lys Thr Ile	
	425	430
	435	
	cta gat agt tta ggc cac tct ctg ctt tac cat aaa ctc gtc cca aaa	1459
	Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His Lys Leu Val Pro Lys	
	440	445
	450	
60	gaa aaa gta cta gca acg gta agg gaa tat tta gaa ttg gta ggg tta	1507
	Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu Glu Leu Val Gly Leu	
	455	460
	465	

21/83

tct gag gag tat ttt tat cgt tat cct cac cag ctt tct gga gga caa Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln Leu Ser Gly Gly Gln 470 475 480 485	1555
caa caa cga gtc tct ata gcg aga gcc cta tta gga gtc cct cag tta Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu Gly Val Pro Gln Leu 490 495 500	1603
10 att att tgt gac gaa att gtt tct gct cta gat tta tct att caa gca Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp Leu Ser Ile Gln Ala 505 510 515	1651
caa att ctg aat atg ctt gcc gag ctg caa aaa aaa ctc agc ctc aca Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys Leu Ser Leu Thr 520 525 530	1699
20 tat ctc ttc att tcg cat gat ctt gcc gtt gta cgc tcg ttc tgc aca Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg Ser Phe Cys Thr 535 540 545	1747
gag gta ttc att atg tat aag ggg caa att gta gaa aaa gga aat aca Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu Lys Gly Asn Thr 550 555 560 565	1795
aaa cgc att ttt tct gat cca caa cat cct tat acg cgc atg ttg tta Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg Met Leu Leu 570 575 580	1843
30 aat gcc caa ctt cca gag act cct gat caa agg caa tct aaa cct ata Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln Ser Lys Pro Ile 585 590 595	1891
ttc caa gaa tat cac aaa gat tct gaa gaa tct tgc tct aca gga tgc Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys Ser Thr Gly Cys 600 605 610	1939
40 tac ttt tac aat cgt tgt cca caa aaa caa gaa gct tgc aag tca gag Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu Ala Cys Lys Ser Glu 615 620 625	1987
atc atc cca aat caa gga gac gcg cac cat aca tac cgt tgt atc cat Ile Ile Pro Asn Gln Gly Asp Ala His His Thr Tyr Arg Cys Ile His 630 635 640 645	2035
tgattcgtcc tctacgctat tcttaagcta ccattaagga atcccaaggg agaggtctgc tctat	2095 2100
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<220> <221> SITE <222> (59)...(67)	
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22/83

<400> 14

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<211> 2300

10 <212> DNA

<213> Chlamydia pneumoniae

<220>

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					Met	Pro	Gly	Ile	Glu	
					1				5	

aaa	gca	gca	aca	aca	gtg	gct	gta	cct	caa	gac	aaa	tct	gaa	gaa	gaa	163
Lys	Ala	Ala	Thr	Thr	Val	Ala	Val	Pro	Gln	Asp	Lys	Ser	Glu	Glu	Glu	
											10	15	20			

30	aaa	gtt	aaa	gag	cga	ttg	aca	aag	cg	gaa	ctt	acc	tgt	gaa	gac	ctt	211
	Lys	Val	Lys	Glu	Arg	Leu	Thr	Lys	Arg	Glu	Leu	Thr	Cys	Glu	Asp	Leu	
											25	30	35				

aaa	gat	aac	ggc	tat	act	gtc	aat	ttt	gaa	gac	att	tct	att	tta	gag	259
Lys	Asp	Asn	Gly	Tyr	Thr	Val	Asn	Phe	Glu	Asp	Ile	Ser	Ile	Leu	Glu	
											40	45	50			

ttg	ttg	cag	ttc	gta	agt	aaa	att	tct	gga	acg	aac	ttt	gtc	ttt	gat	307
Leu	Leu	Gln	Phe	Val	Ser	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Val	Phe	Asp	
											55	60	65			

40	agc	aac	gat	ttg	caa	ttc	aat	gtc	acg	atc	gtt	tcc	cac	gat	cct	act	355
	Ser	Asn	Asp	Leu	Gln	Phe	Asn	Val	Thr	Ile	Val	Ser	His	Asp	Pro	Thr	
											70	75	80	85			

tct	gta	gat	gat	tta	tct	aca	atc	tta	cta	caa	gtc	tta	aaa	atg	cat	403
Ser	Val	Asp	Asp	Leu	Ser	Thr	Ile	Leu	Leu	Gln	Val	Leu	Lys	Met	His	
											90	95	100			

50	gac	ttg	aag	gtt	gtt	gaa	caa	ggc	aat	aac	gtc	ctt	atc	tat	cgt	aat	451
	Asp	Leu	Lys	Val	Val	Glu	Gln	Gly	Asn	Asn	Val	Ile	Tyr	Arg	Asn		
											105	110	115				

cct	cat	ctt	tct	aag	cta	tcc	aca	gta	gtc	aca	gac	agc	tcc	tta	aaa	499
Pro	His	Leu	Ser	Lys	Leu	Ser	Thr	Val	Val	Thr	Asp	Ser	Ser	Leu	Lys	
											120	125	130			

gaa	acg	tgt	gaa	gct	gtt	gtg	gtt	acc	cga	gtg	ttc	cgt	ctt	tac	agg	547
Glu	Thr	Cys	Glu	Ala	Val	Val	Val	Thr	Arg	Val	Phe	Arg	Leu	Tyr	Arg	
											135	140	145			

23/83

	cgt cag ccc tct gca gca gta aat att att caa cct tta ctt tcc cat	595
	Arg Gln Pro Ser Ala Ala Val Asn Ile Ile Gln Pro Leu Leu Ser His	
150	155	160
	165	
	gat gct atc gtt agt gct tca gaa gct act cgt cat gtt atc atc tcg	643
	Asp Ala Ile Val Ser Ala Ser Glu Ala Thr Arg His Val Ile Ile Ser	
170	175	180
10		
	gat att gct ggt aat gtc gat aaa gtc agt gat ttg cta gca gct cta	691
	Asp Ile Ala Gly Asn Val Asp Lys Val Ser Asp Leu Leu Ala Ala Leu	
185	190	195
	gat tgc cca ggc aca tct gtg gac atg act gaa tac gaa gtt aaa tat	739
	Asp Cys Pro Gly Thr Ser Val Asp Met Thr Glu Tyr Glu Val Lys Tyr	
200	205	210
20		
	gcc aat ccc gca gct ctt gtt agc tac tgc caa gat gtt ctt ggt act	787
	Ala Asn Pro Ala Ala Leu Val Ser Tyr Cys Gln Asp Val Leu Gly Thr	
215	220	225
	ctg gcc gaa gat gat gct ttc caa atg ttc atc caa cct gga acg aac	835
	Leu Ala Glu Asp Asp Ala Phe Gln Met Phe Ile Gln Pro Gly Thr Asn	
230	235	240
	245	
	aaa att ttc gtc gtc tct tca cca cgt ctt gca aat aag gca gag cag	883
	Lys Ile Phe Val Val Ser Ser Pro Arg Leu Ala Asn Lys Ala Glu Gln	
250	255	260
30		
	ctc ctg aag tcc tta gat gtc cca gaa atg gca cat acc cta gat gat	931
	Leu Leu Lys Ser Leu Asp Val Pro Glu Met Ala His Thr Leu Asp Asp	
265	270	275
	cct gca agt act gcc ttg gct ttg gga gga aca gga acc acg acg cct	979
	Pro Ala Ser Thr Ala Leu Ala Leu Gly Gly Thr Gly Thr Ser Pro	
280	285	290
40		
	aag agt ttg cgg ttc ttt atg tac aag ctg aag tat caa aat gga gaa	1027
	Lys Ser Leu Arg Phe Phe Met Tyr Lys Leu Lys Tyr Gln Asn Gly Glu	
295	300	305
	gtg att gct aat gcc ctc caa gat atc ggt tac aat cta tat gta acc	1075
	Val Ile Ala Asn Ala Leu Gln Asp Ile Gly Tyr Asn Leu Tyr Val Thr	
310	315	320
	325	
	aca gct atg gac gaa gat ttc att aac act ctc aat agt atc cag tgg	1123
	Thr Ala Met Asp Glu Asp Phe Ile Asn Thr Leu Asn Ser Ile Gln Trp	
330	335	340
50		
	tta gag gtc aat aac tcc ata gtt att atc gga aac caa ggg aat gtc	1171
	Leu Glu Val Asn Asn Ser Ile Val Ile Ile Gly Asn Gln Gly Asn Val	
345	350	355
	gac aga gtt att ggc ctc tta aac ggt tta gat tta cct cct aaa cag	1219
	Asp Arg Val Ile Gly Leu Leu Asn Gly Leu Asp Leu Pro Pro Lys Gln	
360	365	370
60		
	gtt tac atc gaa gtt tta att cta gat acc agc tta gag aaa tcc tgg	1267
	Val Tyr Ile Glu Val Leu Ile Leu Asp Thr Ser Leu Glu Lys Ser Trp	
375	380	385

24/83

gac ttt gga gtg caa tgg gta gcc cta ggt gat gaa caa agt aaa gta Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp Glu Gln Ser Lys Val 390 395 400 405	1315
gct tat gct tct gga cta ttg aat aat act ggc ata gcc aca cct aca Ala Tyr Ala Ser Gly Leu Leu Asn Asn Thr Gly Ile Ala Thr Pro Thr 410 415 420	1363
10 aaa gca act gtc cct ccc ggc acg cca aat cct ggt tcg atc cct ctt Lys Ala Thr Val Pro Pro Gly Thr Pro Asn Pro Gly Ser Ile Pro Leu 425 430 435	1411
cct acg cca gga caa ttg aca ggg ttc tca gat atg ctg aac tct tcg Pro Thr Pro Gly Gln Leu Thr Gly Phe Ser Asp Met Leu Asn Ser Ser 440 445 450	1459
20 tca gca ttc ggt cta gga atc atc gga aat gtc cta agt cat aaa ggg Ser Ala Phe Gly Leu Gly Ile Ile Gly Asn Val Leu Ser His Lys Gly 455 460 465	1507
aag tct ttc ctt act ttg gga ggc tta tta agt gcc tta gat caa gat Lys Ser Phe Leu Thr Leu Gly Leu Leu Ser Ala Leu Asp Gln Asp 470 475 480 485	1555
gga gat act gtc att gtc ttg aat cct aga atc atg gct cag gat acg Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile Met Ala Gln Asp Thr 490 495 500	1603
30 caa caa gct tcg ttt ttt gta ggg caa acg gtc cct tac caa act atc Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val Pro Tyr Gln Thr Ile 505 510 515	1651
aaa tac tat atc caa gaa aca gga act gta acg caa aat atc gat tat Lys Tyr Tyr Ile Gln Glu Thr Gly Thr Val Thr Gln Asn Ile Asp Tyr 520 525 530	1699
40 gaa gat att gga gtg aac ctt gtc gtt acc tct aca gtt gct ccc aac Glu Asp Ile Gly Val Asn Leu Val Val Thr Ser Thr Val Ala Pro Asn 535 540 545	1747
aat gta gtt aca cta caa atc gaa cag acg atc tca gaa tta cat tcc Asn Val Val Thr Leu Gln Ile Glu Gln Thr Ile Ser Glu Leu His Ser 550 555 560 565	1795
gcg tct gga tca cta aca cct gtc aca gat aaa act tat gca gcc aca Ala Ser Gly Ser Leu Thr Pro Val Thr Asp Lys Thr Tyr Ala Ala Thr 570 575 580	1843
50 cgc tta caa att ccc gac ggt tgt ttc tta gtt atg agt ggg cat atc Arg Leu Gln Ile Pro Asp Gly Cys Phe Leu Val Met Ser Gly His Ile 585 590 595	1891
aga gat aaa act aca aaa gtg gtt tca gga gtg cct ttg cta aac tcc Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val Pro Leu Leu Asn Ser 600 605 610	1939
60 ata cca tta att cgt ggt tta ttt agc cgt acc atc gac caa agg caa Ile Pro Leu Ile Arg Gly Leu Phe Ser Arg Thr Ile Asp Gln Arg Gln 615 620 625	1987

25/83

aaa cgc aat atc atg atg ttt att aag cct aag gtg att agt agc ttt 2035
 Lys Arg Asn Ile Met Met Phe Ile Lys Pro Lys Val Ile Ser Ser Phe
 630 635 640 645

 gaa gaa ggc act cgt gtt acc aat aag gaa gga tac aga tac aat tgg 2083
 Glu Glu Gly Thr Arg Val Thr Asn Lys Glu Gly Tyr Arg Tyr Asn Trp
 650 655 660
 10 gaa gct gat gaa gga tcc atg caa gtg gcc cct cgc cat gct cct gaa 2131
 Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro Arg His Ala Pro Glu
 665 670 675

 tgc caa gga cct cct tct tta cag gct gaa agt gac ttt aaa ata ata 2179
 Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser Asp Phe Lys Ile Ile
 680 685 690

 gaa ata gaa gct cag tagtggtata taaaagagga agatgatatt ctccgccgtg 2234
 20 Glu Ile Glu Ala Gln
 695

 gaatagcttc tgactctgtt gcattcaggg ggaaagccaa gaagatgtag agtcggccgt 2294
 ataact 2300

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 30 <213> Chlamydia pneumoniae

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 <222> (50)..(58)

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 1 5

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 Met Ser Arg Lys Asp
 1 5

 aat gag gtt tcc tta gct cgt tca att ttt aat ata tta tcc gga act 163
 Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn Ile Leu Ser Gly Thr
 10 15 20
 60

26/83

	ttc tgt agt cgt att aca ggg ata ttt cga gaa att gca atg gca acc Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu Ile Ala Met Ala Thr 25 30 35	211
	tat ttt gga gct gat cca att gta gct gct ttc tgg tta ggt ttc cgt Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe Trp Leu Gly Phe Arg 40 45 50	259
10	act gtt ttt ttc tta aga aaa att tta gga ggg ctc att cta gaa caa Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly Leu Ile Leu Glu Gln 55 60 65	307
	gcc ttc atc cct cat ttt gaa ttt ctc cgt gct caa agt ctc gat cgt Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala Gln Ser Leu Asp Arg 70 75 80 85	355
20	gcg gcg ttt ttt ttc cga cgc ttt tct aga ttg att aaa ggc agc act Ala Ala Phe Phe Arg Arg Phe Ser Arg Leu Ile Lys Gly Ser Thr 90 95 100	403
	att ata ttc act ctg ctt att gaa gca gta ttg tgg gta ttc ttc aat Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu Trp Val Phe Phe Asn 105 110 115	451
	aac gtt gaa gag ggg act tac gat atg att ctc ctt act atg ata ctc Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu Leu Thr Met Ile Leu 120 125 130	499
30	ttg ccc tgt ggc att ttc tta atg atg tac aat gta aac ggc gct ttg Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn Val Asn Gly Ala Leu 135 140 145	547
	ctt cac tgt gga aat aag ttt ttc ggg gtg gga tta gct ccc gta gtt Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly Leu Ala Pro Val Val 150 155 160 165	595
40	gta aat atc att tgg att ttc ttt gtt ata gcg gct cgt cat tca gat Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala Ala Arg His Ser Asp 170 175 180	643
	cct aga gag cgt att atc ggt tta tcc gtg gct cta gtt atc ggg ttt Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala Leu Val Ile Gly Phe 185 190 195	691
	ttc ttc gaa tgg tta atc acg gtt cct gga gta tgg aaa ttt cta tta Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val Trp Lys Phe Leu Leu 200 205 210	739
50	gaa gcg aag agc cca cct caa gaa cac gat agt gtt cga gct tta tta Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser Val Arg Ala Leu Leu 215 220 225	787
	gct ccc tta tct ttg ggt att tta act tca agc atc ttc cag ctg aac Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser Ile Phe Gln Leu Asn 230 235 240 245	835
60	ctt ctt tct gat atc tgc ttg gct cgc tat gta cat gaa ata ggc cct Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val His Glu Ile Gly Pro 250 255 260	883

27/83

	ctt tat ctt atg tac tcc tta aag att tat cag ctc ccc ata cat ctc Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln Leu Pro Ile His Leu 265 270 275	931
	ttt ggc ttt ggt gtg ttt acc gtt ctc ctc cca gca att tct cgt tgt Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro Ala Ile Ser Arg Cys 280 285 290	979
10	gta cag cga gaa gat cat gag agg gga ttg aaa ctt atg aag ttc gtt Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys Leu Met Lys Phe Val 295 300 305	1027
	ctc acc cta acc atg tcc gta atg atc att atg aca gca ggg cta ttg Leu Thr Leu Thr Met Ser Val Met Ile Ile Met Thr Ala Gly Leu Leu 310 315 320 325	1075
20	ctc tta gct tta cct gga gtc cgt gtc ctt tat gaa cac gga ctt ttc Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr Glu His Gly Leu Phe 330 335 340	1123
	cct cag agt gct gtc tac gct att gtt cgt gta ttg cga ggt tat ggt Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val Leu Arg Gly Tyr Gly 345 350 355	1171
	gcc agt att atc cct atg gcc ttg gct cct tta gtc tct gtt ctt ttt Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu Val Ser Val Leu Phe 360 365 370	1219
30	tat gca cag cgg cag tat gct gtt ccg ctc ttt ata gga atc ggt acg Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe Ile Gly Ile Gly Thr 375 380 385	1267
	gct ttg gcc aat att gtt tta agc ttg gtt cta ggt cgt tgg gtt tta Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu Gly Arg Trp Val Leu 390 395 400 405	1315
40	aaa gac gtc tcg ggc att tcc tat gct aca tcc ata act gct tgg gtg Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser Ile Thr Ala Trp Val 410 415 420	1363
	cag tta tat ttc ctc tgg tat tat tct tcg aaa aga ctc cct atg tac Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys Arg Leu Pro Met Tyr 425 430 435	1411
	tct aag tta ctt tgg gag agc atc cgg cgt tcc ata aaa gtt atg gga Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser Ile Lys Val Met Gly 440 445 450	1459
50	acc act atg ctt gct tgt atg att act cta ggc tta aat atc ctt acg Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly Leu Asn Ile Leu Thr 455 460 465	1507
	caa act aca tat gta att ttc tta aac ccc ctc aca cca ctt gct tgg Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu Thr Pro Leu Ala Trp 470 475 480 485	1555
60	ccc tta tcc tcc ata acg gct caa gca att gct ttt tta tct gag agc Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala Phe Leu Ser Glu Ser 490 495 500	1603

28/83

tgc att ttc ttg gct ttt ttg ttt ggt ttt gca aaa ctg ctt cga gta 1651
 Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu Leu Arg Val
 505 510 515

gaa gat ctt att aat ttg gct tct ttt gaa tac tgg cgt ggg caa cg 1699
 Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg Gly Gln Arg
 520 525 530

10 ggt ctt ttg caa aga caa cac gtg atg caa gac act caa aat 1741
 Gly Leu Leu Gln Arg Gln His Val Met Gln Asp Thr Gln Asn
 535 540 545

taatcatgtt tggttcttgt agctcagtcg ctttctttta gcttaagtt ttgatagcct 1801
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 Met Lys Thr Ser Arg
 1 5

50 aat aaa cag tgc aaa ata aca gat ccc tta agt aaa tct tcc ttc ttt 163
 Asn Lys Gln Cys Lys Ile Thr Asp Pro Leu Ser Lys Ser Ser Phe Phe
 10 15 20

gtt gga gcc tta att tta ggt aaa act aca ata ctc ctt aat gcg act 211
 Val Gly Ala Leu Ile Leu Gly Lys Thr Thr Ile Leu Leu Asn Ala Thr
 25 30 35

ccg ttg tct gac tat ttt gat aat caa gca aat caa ctc aca aca ctc 259
 Pro Leu Ser Asp Tyr Phe Asp Asn Gln Ala Asn Gln Leu Thr Thr Leu
 60 40 45 50

29/83

	ttc cct cta att gat act ctt act aac atg act ccc tac tct cat aga	307	
	Phe Pro Leu Ile Asp Thr Leu Thr Asn Met Thr Pro Tyr Ser His Arg		
55	55	60	
	55	65	
	gca aca ctt ttt gga gtt agg gat gac act aac caa gac att gtc ctc	355	
	Ala Thr Leu Phe Gly Val Arg Asp Asp Thr Asn Gln Asp Ile Val Leu		
70	70	75	
	70	80	
	70	85	
10	gat cac cag aat tcc ata gaa agc tgg ttc gaa aac ttc tct caa gac	403	
	Asp His Gln Asn Ser Ile Glu Ser Trp Phe Glu Asn Phe Ser Gln Asp		
	90	95	100
	90	95	100
	ggc ggt gct ctc tct tgc aaa tca ctt gcc ata acg aat aca aaa aac	451	
	Gly Gly Ala Leu Ser Cys Lys Ser Leu Ala Ile Thr Asn Thr Lys Asn		
	105	110	115
20	caa att ctt ttc cta aat agc ttt gct att aaa aga gct ggt gcg atg	499	
	Gln Ile Leu Phe Leu Asn Ser Phe Ala Ile Lys Arg Ala Gly Ala Met		
	120	125	130
	120	125	130
	tat gtt gat ggt aat ttc gat ctt tct gag aat cat ggt tcc atc att	547	
	Tyr Val Asp Gly Asn Phe Asp Leu Ser Glu Asn His Gly Ser Ile Ile		
	135	140	145
	135	140	145
	ttc tct ggg aat tta agc ttt cct aat gca agt aat ttc gct gat act	595	
	Phe Ser Gly Asn Leu Ser Phe Pro Asn Ala Ser Asn Phe Ala Asp Thr		
30	150	155	160
	150	155	160
	150	155	160
	tgt aca ggg gga gct gtt tta tgt tcg aaa aat gtt aca atc tca aaa	643	
	Cys Thr Gly Gly Ala Val Leu Cys Ser Lys Asn Val Thr Ile Ser Lys		
	170	175	180
	170	175	180
	aat caa gga acc gca tac ttc att aac aac aag gca aaa tct tca gga	691	
	Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys Ala Lys Ser Ser Gly		
	185	190	195
	185	190	195
40	gga gca atc caa gct gca atc ata aac att aag gac aac act ggc cct	739	
	Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys Asp Asn Thr Gly Pro		
	200	205	210
	200	205	210
	tgc ctg ttt ttt aat aat gct gca ggc gga aca gcg ggg ggc gcg ttg	787	
	Cys Leu Phe Asn Asn Ala Ala Gly Gly Thr Ala Gly Gly Ala Leu		
	215	220	225
	215	220	225
	ttc gct aat gct tgt aga att gag aat aat tct cag cct atc tat ttt	835	
	Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser Gln Pro Ile Tyr Phe		
50	230	235	240
	230	235	240
	ttg aat aac caa tca ggt ctg ggt gca ata aga gta cat caa gag	883	
	Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile Arg Val His Gln Glu		
	250	255	260
	250	255	260
	tgc att ctt aca aag aat acc ggt tct gtg atc ttc aac aat aat ttt	931	
	Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile Phe Asn Asn Asn Phe		
	265	270	275
	265	270	275
60	gcc atg gaa gcg gac atc tct gct aac cat tcc tct gga ggg gct atc	979	
	Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser Ser Gly Gly Ala Ile		
	280	285	290
	280	285	290

30/83

	tat tgc att agt tgt tct ata aaa gac aac cca gga att gca gcc ttc Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro Gly Ile Ala Ala Phe 295 300 305	1027
	gat aat aat act gca gca cga gat gga ggt gct atc tgt aca caa tct Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala Ile Cys Thr Gln Ser 310 315 320 325	1075
10	cta act ata caa gac agt ggt ccc gtc tat ttc aca aac aat cag gga Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe Thr Asn Asn Gln Gly 330 335 340	1123
	act tgg ggc ggc gct atc atg ctc cgt caa gat ggt gca tgc act tta Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp Gly Ala Cys Thr Leu 345 350 355	1171
20	ttt gct gat cag gga gat att att ttt tat aat aat aga cac ttc aaa Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn Asn Arg His Phe Lys 360 365 370	1219
	gat act ttc agc aat cat gtt tct gta aac tgc acg cgt aat gtc tca Asp Thr Phe Ser Asn His Val Ser Val Asn Cys Thr Arg Asn Val Ser 375 380 385	1267
	tta aca gtt gga gca agt caa ggt cat tct gct acc ttc tat gat ccc Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala Thr Phe Tyr Asp Pro 390 395 400 405	1315
30	ata cta caa aga tat act ata caa aac tct atc caa aaa ttt aat cct Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile Gln Lys Phe Asn Pro 410 415 420	1363
	aat cca gaa cac ctc gga act atc ttg ttc tcc tca aca tat att ccg Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser Ser Thr Tyr Ile Pro 425 430 435	1411
40	gat aca tcg act tct cgt gat gac ttc att tca cat ttc aga aac cac Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser His Phe Arg Asn His 440 445 450	1459
	att gga ctg tac aac ggc aca ctc gct ctt gaa gat cga gca gag tgg Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu Asp Arg Ala Glu Trp 455 460 465	1507
	aaa gtc tat aaa ttt gat caa ttt ggt ggg act cta cgg tta ggc agt Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr Leu Arg Leu Gly Ser 470 475 480 485	1555
50	aga gct gtg ttt tct aca aca gac gaa gaa caa agt agc agt agt gtg Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln Ser Ser Ser Val 490 495 500	1603
	ggt tct gta att aac atc aat aat ctt gca att aac ctt ccc tct atc Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile 505 510 515	1651
60	tta ggc aac aga gtt gct ccc aag cta tgg att cgc ccc aca ggt tca Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile Arg Pro Thr Gly Ser 520 525 530	1699

31/83

	tca gca ccc tat agc gaa gat aat aac cct ata atc aat ctc tca gga Ser Ala Pro Tyr Ser Glu Asp Asn Asn Pro Ile Ile Asn Leu Ser Gly 535 540 545	1747
	cct ttg agc cta ctg gat gac gag aac cta gat ccc tat gat act gca Pro Leu Ser Leu Leu Asp Asp Glu Asn Leu Asp Pro Tyr Asp Thr Ala 550 555 560 565	1795
10	gac ctt gcc caa cct atc gca gaa gtt cct ctg tat ctc tta gac Asp Leu Ala Gln Pro Ile Ala Glu Val Pro Leu Leu Tyr Leu Leu Asp 570 575 580	1843
	gtc aca gct aaa cat att aat acg gat aat ttc tac cct gag ggt cta Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe Tyr Pro Glu Gly Leu 585 590 595	1891
20	aat aca act caa cac tac ggc tac caa ggc gtt tgg tcc cct tac tgg Asn Thr Gln His Tyr Gly Tyr Gln Gly Val Trp Ser Pro Tyr Trp 600 605 610	1939
	atc gaa aca atc aca act tct gat acc tct tct gaa gat act gtg aat Ile Glu Thr Ile Thr Ser Asp Thr Ser Ser Glu Asp Thr Val Asn 615 620 625	1987
	act tta cat cgc cag ctt tat ggt gat tgg aca cct aca gga tat aag Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr Pro Thr Gly Tyr Lys 630 635 640 645	2035
30	gta aac cca gaa aac aaa gga gac att gcc cta tct gcc ttc tgg caa Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu Ser Ala Phe Trp Gln 650 655 660	2083
	tct ttc cat aac tta ttt gcg aca cta cgt tat caa aca cag caa ggc Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr Gln Thr Gln Gly 665 670 675	2131
40	caa ata gca cct aca gct tct gga gaa gct act cga ctc ttc gtg cat Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr Arg Leu Phe Val His 680 685 690	2179
	caa aat agc aac aat gat gcg aaa gga ttc cat atg gaa gct acg ggt Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His Met Glu Ala Thr Gly 695 700 705	2227
	tat tct ttg gga aca acc tca aac act gct tct aat cat agc ttt ggt Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser Asn His Ser Phe Gly 710 715 720 725	2275
50	gta aac ttc tcc caa ctt ttc agt aat ctc tac gag agc cac tcc gac Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr Glu Ser His Ser Asp 730 735 740	2323
	aat tcc gtg gct tcg cat acg aca act gta gcg ctc cag atc aat aat Asn Ser Val Ala Ser His Thr Thr Val Ala Leu Gln Ile Asn Asn 745 750 755	2371
60	cct tgg ctg caa gag aga ttc tct aca tct gca tct cta gcc tac agc Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala Ser Leu Ala Tyr Ser 760 765 770	2419

32/83

	tac agc aac cac cat atc aaa gca tct gga tat tct gga aaa ata caa Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr Ser Gly Lys Ile Gln 775 780 785	2467
	acg gaa ggc aaa tgt tat agt acg aca tta ggg gcg gct ctc tct tgc Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly Ala Ala Leu Ser Cys 790 795 800 805	2515
10	tct cta tct cta caa tgg cga tca cga cct ctc cac ttc act cct ttt Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro Leu His Phe Thr Pro Phe 810 815 820	2563
	atc caa gca att gcc gtt cgt tct aat caa act gcg ttt caa gaa agt Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr Ala Phe Gln Glu Ser 825 830 835	2611
20	gga gat aaa gct aga aaa ttt tct gtt cat aaa ccc tta tat aac ctg Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys Pro Leu Tyr Asn Leu 840 845 850	2659
	aca gtc cct ctg gga att cag agc gct tgg gaa tcc aag ttc cgt ctt Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu Ser Lys Phe Arg Leu 855 860 865	2707
	cct acc tat tgg aac ata gag ctt gct tat cag cct gtc ctc tac caa Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln Pro Val Leu Tyr Gln 870 875 880 885	2755
30	caa aat cct gag atc aac gtg agt cta gaa tct agt gga tcg tca tgg Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser Ser Gly Ser Ser Trp 890 895 900	2803
	ctc cta tca gga acc acc ctt gct cgc aat gcc att gct ttt aaa gga Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala Ile Ala Phe Lys Gly 905 910 915	2851
40	aga aac caa att ttt atc ttc cct aaa ctt tcg gtg ttc tta gac tat Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser Val Phe Leu Asp Tyr 920 925 930	2899
	caa ggc tcg gta tcc tca tca acg acg aca cat tac ctt cac gca gga Gln Gly Ser Val Ser Ser Thr Thr His Tyr Leu His Ala Gly 935 940 945	2947
	acg acc ttt aag ttt taaaagcatg ttatataagac aatgcaacct gtaaaagacca Thr Thr Phe Lys Phe 950	3002
50	aatagagagt agtgaacact ctctaccatc atgaatctta tgggagaagc taagggaaat 3062 ccacagatac gttccccca taaaaattaa gaacccgata catcctcaact agagattcga 3122 aagaactact taaatcctaa gcattcga 3150	

<210> 20
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<212> PRT
<213> Chlamydia pneumoniae
60 <220>

<221> SITE
<222> (119)..(127)

<400> 20
Ile Leu Phe Leu Asn Ser Phe Ala Ile
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10

<210> 21
<211> 3200
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(3100)

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cactctctcc ttagattact ctgcggatat ttccctctcc acgctgagtc actacttaaa 180
cgtggcgagt agaatgagat tttaacaat aagtgaccaa aacagaaaaga ttaaggaacc 240
tctagtgtca aagactcctc ctaagtttt attctatctc gggatttca cagcctgcatt 300
gttcgggatg actctgcag tgtatagttt acaaacggac tcccttggaaa agtttgcatt 360
agagagggat gaagagttt gcacgagctt tcctcttta gactctctt ccactcttac 420
aggattttct ccaataacta cgtttggaa aaatagacat aattctctc aagacattgt 480
actttctaac tacaagtcta ttgataaacat ccttcttctt tggacatcgg ctgggggagc 540

30 tttgtcctgt aataattttct tattataaaa ttgttgaagac catgccttct tcagtaaaaa 600
tctcgcgatt gggactggag gcgcgattgc ttgcaggga gcctgcacaa tcacgaagaa 660
tagaggaccc cttatTTTT tcagcaatcg aggtcttaac aatgcggagta caggaggaga 720
aactcggtgg ggtgcgatttgc cctgtatgg agacttcacg atttctcaaa atcaaggagc 780
tttctacttt gtcaacaatt ccgtcaacaa ctggggagga gccccttcca ccaatggaca 840
ctgcgcgcattt caaagcaaca gggcaccttactctttttt aacaatacag cccctagtgg 900
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ggcgagtatt gcaacaactg ccaactctga gactccatca actagtgttag gctcccagg 1740

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 aaaatggcag tcaaaattcc acgtacacctac agaatggact ctagaacttt cttaccaacc 2880
 10 ggtactctat caacaaaatc cccaaatcgg tgcacgcta cttgcgagcg gaggttcctg 2940
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 tgcgctcttc cgttctctcg atctattctt ggattaccaa ggatcggtct ctcctcgac 3060
 atctacgcac catctccaag caggaagtac cttaaaattc taaaataaaaaa gaacgataaaa 3120
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<210> 22
<211> 9
20 <212> PRT
<213> Chlamydia pneumoniae

<220>
<221> SITE
<222> (56)..(64)

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1 5

30 <210> 23
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<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(2893)

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tttctatting tgaacgagta tgcgcttttt ttgcttcgga atg ttg ctt cct ttt 115
Met Leu Leu Pro Phe
1 5

.act ttt gta ttg gct aat gaa ggt ctc caa ctt cct ttg gag acc tat 163
Thr Phe Val Leu Ala Asn Glu Gly Leu Gln Leu Pro Leu Glu Thr Tyr
50 10 . 15 20

att aca tta agt cct gaa tat caa gca gcc cct caa gta ggg ttt act 211
Ile Thr Leu Ser Pro Glu Tyr Gln Ala Ala Pro Gln Val Gly Phe Thr
25 30 35

cat aac caa aat caa gat ctc gca att gtc ggg aat cac aat gat ttc 259
His Asn Gln Asn Gln Asp Leu Ala Ile Val Gly Asn His Asn Asp Phe
40 45 50

	atc ttg gac tat aag tac tat cgg tcg aat gga ggt gct ctt acc tgt Ile Leu Asp Tyr Lys Tyr Tyr Arg Ser Asn Gly Gly Ala Leu Thr Cys 55 60 65	307
	aag aat ctt ctg atc tct gaa aat ata ggg aat gtc ttc ttt gag aag Lys Asn Leu Leu Ile Ser Glu Asn Ile Gly Asn Val Phe Phe Glu Lys 70 75 80 85	355
10	aat gtc tgt ccc aat tct ggc ggg gca att tat gct gct caa aat tgc Asn Val Cys Pro Asn Ser Gly Gly Ala Ile Tyr Ala Ala Gln Asn Cys 90 95 100	403
	acg atc tcc aag aat cag aac tat gca ttt act aca aac ttg gtc tct Thr Ile Ser Lys Asn Gln Asn Tyr Ala Phe Thr Thr Asn Leu Val Ser 105 110 115	451
20	gac aat cct aca gcc act gcg gga tca cta ttg ggt gga gct ctc ttt Asp Asn Pro Thr Ala Thr Ala Gly Ser Leu Leu Gly Gly Ala Leu Phe 120 125 130	499
	gcc ata aat tgc tct att act aat aac cta gga cag gga act ttc gtt Ala Ile Asn Cys Ser Ile Thr Asn Asn Leu Gly Gln Gly Thr Phe Val 135 140 145	547
	gac aat ctc gct tta aat aag ggg ggt gcc ctc tat act gag acg aac Asp Asn Leu Ala Leu Asn Lys Gly Gly Ala Leu Tyr Thr Glu Thr Asn 150 155 160 165	595
30	tta tct att aaa gac aat aaa ggc ccg atc ata atc aag cag aat cgg Leu Ser Ile Lys Asp Asn Lys Gly Pro Ile Ile Ile Lys Gln Asn Arg 170 175 180	643
	gca cta aat tcg gac agt tta gga gga ggg att tat agt ggg aac tct Ala Leu Asn Ser Asp Ser Leu Gly Gly Ile Tyr Ser Gly Asn Ser 185 190 195	691
40	cta aat ata gag gga aat tct gga gct ata cag atc aca agc aac tct Leu Asn Ile Glu Gly Asn Ser Gly Ala Ile Gln Ile Thr Ser Asn Ser 200 205 210	739
	tca gga tct ggg gga ggc ata ttt tct acc caa aca ctc acg atc tcc Ser Gly Ser Gly Gly Ile Phe Ser Thr Gln Thr Leu Thr Ile Ser 215 220 225	787
	tcg aat aaa aaa ctc ata gaa atc agt gaa aat tcc gcg ttc gca aat Ser Asn Lys Lys Leu Ile Glu Ile Ser Glu Asn Ser Ala Phe Ala Asn 230 235 240 245	835
50	aac tat gga tcg aac ttc aat cca gga gga gga ggt ctt act acc acc Asn Tyr Gly Ser Asn Phe Asn Pro Gly Gly Gly Leu Thr Thr Thr 250 255 260	883
	ttt tgc acg ata ttg aac aac cga gaa ggg gta ctc ttt aac aat aac Phe Cys Thr Ile Leu Asn Asn Arg Glu Gly Val Leu Phe Asn Asn Asn 265 270 275	931
60	caa agc cag agc aac ggt gga gcc att cat gcg aaa tct atc att atc Gln Ser Gln Ser Asn Gly Gly Ala Ile His Ala Lys Ser Ile Ile Ile 280 285 290	979

	aaa gaa aat ggt cct gta tac ttt tta aat aac act gca act cg ^g gga	1027
	Lys Glu Asn Gly Pro Val Tyr Phe Leu Asn Asn Thr Ala Thr Arg Gly	
	295 300 305	
	ggg gct ctc ctc aac tta tca gca ggt tct gga aac gga agc ttc atc	1075
	Gly Ala Leu Leu Asn Leu Ser Ala Gly Ser Gly Asn Gly Ser Phe Ile	
	310 315 320 325	
10	tta tct gca gat aat gga gat att atc ttt aac aat aat acg gcc tcc	1123
	Leu Ser Ala Asp Asn Gly Asp Ile Ile Phe Asn Asn Asn Thr Ala Ser	
	330 335 340	
	aag cat gcc ctc aat cct cca tac aga aac gcc att cac tcg act cct	1171
	Lys His Ala Leu Asn Pro Pro Tyr Arg Asn Ala Ile His Ser Thr Pro	
	345 350 355	
20	aat atg aat ctg caa ata gga gcc cgt ccc ggc tat cga gtg ctg ttc	1219
	Asn Met Asn Leu Gln Ile Gly Ala Arg Pro Gly Tyr Arg Val Leu Phe	
	360 365 370	
	tat gat ccc ata gaa cat gag ctc cct tcc tcc ttc ccc ata ctc ttt	1267
	Tyr Asp Pro Ile Glu His Glu Leu Pro Ser Ser Phe Pro Ile Leu Phe	
	375 380 385	
	aat ttc gaa acc ggt cat aca ggt aca gtt tta ttt tca ggg gaa cat	1315
	Asn Phe Glu Thr Gly His Thr Gly Val Leu Phe Ser Gly Glu His	
	390 395 400 405	
30	gta cac cag aac ttt acc gat gaa atg aat ttc ttt tcc tat tta agg	1363
	Val His Gln Asn Phe Thr Asp Glu Met Asn Phe Phe Ser Tyr Leu Arg	
	410 415 420	
	aac act tcg gaa cta cgt caa gga gtc ctt gct gtt gaa gat ggt gcg	1411
	Asn Thr Ser Glu Leu Arg Gln Gly Val Leu Ala Val Glu Asp Gly Ala	
	425 430 435	
40	ggg ctg gcc tgc tat aag ttc ttc caa cga gga ggc act cta ctt cta	1459
	Gly Leu Ala Cys Tyr Lys Phe Phe Gln Arg Gly Thr Leu Leu Leu	
	440 445 450	
	ggt caa ggt gcg gtg atc acg aca gca gga acg att ccc aca cca tcc	1507
	Gly Gln Gly Ala Val Ile Thr Thr Ala Gly Thr Ile Pro Thr Pro Ser	
	455 460 465	
	tca aca cca acg aca gta gga agt act ata act tta aat cac att gcc	1555
	Ser Thr Pro Thr Thr Val Gly Ser Thr Ile Thr Leu Asn His Ile Ala	
	470 475 480 485	
50	att gac ctt cct tct att ctt tct ttt caa gct cag gct cca aaa att	1603
	Ile Asp Leu Pro Ser Ile Leu Ser Phe Gln Ala Gln Ala Pro Lys Ile	
	490 495 500	
	tgg att tac ccc aca aaa aca gga tct acc tat act gaa gat tcc aac	1651
	Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr Thr Glu Asp Ser Asn	
	505 510 515	
60	ccg aca atc aca atc tca gga act ctc acc tta cgc aac agc aac aac	1699
	Pro Thr Ile Thr Ile Ser Gly Thr Leu Thr Leu Arg Asn Ser Asn Asn	
	520 525 530	

	gaa gat ccc tac gat agt ctg gat ctc tcg cac tct ctt gag aaa gtt Glu Asp Pro Tyr Asp Ser Leu Asp Leu Ser His Ser Leu Glu Lys Val 535 540 545	1747
	ccc ctt ctt tat att gtc gat gtc gct gca caa aaa att aac tct tcg Pro Leu Leu Tyr Ile Val Asp Val Ala Ala Gln Lys Ile Asn Ser Ser 550 555 560 565	1795
10	caa ctg gat cta tcc aca tta aat tct ggc gaa cac tat ggg tat caa Gln Leu Asp Leu Ser Thr Leu Asn Ser Gly Glu His Tyr Gly Tyr Gln 570 575 580	1843
	ggc atc tgg tcg acc tat tgg gta gaa act aca aca atc acg aac cct Gly Ile Trp Ser Thr Tyr Trp Val Glu Thr Thr Thr Ile Thr Asn Pro 585 590 595	1891
20	aca tct cta cta ggc gcg aat aca aaa cac aag ctg ctc tat gca aac Thr Ser Leu Leu Gly Ala Asn Thr Lys His Lys Leu Leu Tyr Ala Asn 600 605 610	1939
	tgg tct cct cta ggc tac cgt cct cat ccc gaa cgt cga gga gaa ttc Trp Ser Pro Leu Gly Tyr Arg Pro His Pro Glu Arg Arg Gly Glu Phe 615 620 625	1987
	att acg aat gcc ttg tgg caa tcg gca tat acg gct ctt gca gga ctc Ile Thr Asn Ala Leu Trp Gln Ser Ala Tyr Thr Ala Leu Ala Gly Leu 630 635 640 645	2035
30	cac tcc ctc tcc tcc tgg gat gaa gag aag ggt cat gca gct tcc cta His Ser Leu Ser Ser Trp Asp Glu Glu Lys Gly His Ala Ala Ser Leu 650 655 660	2083
	caa ggc att ggt ctt ctg gtt cat caa aaa gac aaa aac ggt ttt aag Gln Gly Ile Gly Leu Leu Val His Gln Lys Asp Lys Asn Gly Phe Lys 665 670 675	2131
40	gga ttt cgt agt cat atg aca ggt tat agt gct acc acc gaa gca acc Gly Phe Arg Ser His Met Thr Gly Tyr Ser Ala Thr Thr Glu Ala Thr 680 685 690	2179
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	aaa gct aaa gaa cat gaa tct caa aat agc acg tcc tct cac cac tat Lys Ala Lys Glu His Glu Ser Gln Asn Ser Thr Ser Ser His His Tyr 710 715 720 725	2275
50	ttc tct gga atg tgc ata gca aaa tac tct ctt caa aga gtg ata cgt Phe Ser Gly Met Cys Ile Ala Lys Tyr Ser Leu Gln Arg Val Ile Arg 730 735 740	2323
	cta tct gtg tct ctt gct tat atg ttt acc tcg gaa cat acc cat aca Leu Ser Val Ser Leu Ala Tyr Met Phe Thr Ser Glu His Thr His Thr 745 750 755	2371
60	atg tat cag ggt ctc ctg gaa ggg aac tct cag gga tct ttc cac aac Met Tyr Gln Gly Leu Leu Glu Gly Asn Ser Gln Gly Ser Phe His Asn 760 765 770	2419

38/83

	cat acc tta gca ggg gct ctc tcc tgt gtt ttc tta cct caa cct cac His Thr Leu Ala Gly Ala Leu Ser Cys Val Phe Leu Pro Gln Pro His 775 780 785	2467
	ggc gag tcc ctg cag atc tat ccc ttt att act gcc tta gcc atc cga Gly Glu Ser Leu Gln Ile Tyr Pro Phe Ile Thr Ala Leu Ala Ile Arg 790 795 800 805	2515
10	gga aat ctt gct gcg ttt caa gaa tct gga gac cat gct cgg gaa ttt Gly Asn Leu Ala Ala Phe Gln Glu Ser Gly Asp His Ala Arg Glu Phe 810 815 820	2563
	tcc cta cac cgc ccc cta acg gac gtc tcc ctc cct gta gga atc cgc Ser Leu His Arg Pro Leu Thr Asp Val Ser Leu Pro Val Gly Ile Arg 825 830 835	2611
20	gct tct tgg aag aac cac cac cga gtt ccc cta gtc tgg ctc aca gaa Ala Ser Trp Lys Asn His His Arg Val Pro Leu Val Trp Leu Thr Glu 840 845 850	2659
	att tcc tat cgc tct act ctc tat agg caa gat cct gaa ctc cac tcg Ile Ser Tyr Arg Ser Thr Leu Tyr Arg Gln Asp Pro Glu Leu His Ser 855 860 865	2707
	aaa tta ctg att agc caa ggt acg tgg acg acg cag gcc act cct gtg Lys Leu Leu Ile Ser Gln Gly Thr Trp Thr Thr Gln Ala Thr Pro Val 870 875 880 885	2755
30	acc tac aat gct tta ggg atc aaa gtg aaa aat acc atg cag gtg ttt Thr Tyr Asn Ala Leu Gly Ile Lys Val Lys Asn Thr Met Gln Val Phe 890 895 900	2803
	cct aaa gtc act ctc tcc tta gat tac tct gcg gat att tct tcc tcc Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp Ile Ser Ser Ser 905 910 915	2851
40	acg ctg agt cac tac tta aac gtg gcg agt aga atg aga ttt Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg Met Arg Phe 920 925 930	2893
	taacaataag tgacccaaac agaaaagatta aggaacctct agtgtcaaag actcctcccta 2953 agtttttatt ctatctcgaa aatttcacag cctgcattt cggatg 3000	
	<210> 24	
	<211> 9	
	<212> PRT	
50	<213> Chlamydia pneumoniae	
	<220>	
	<221> SITE	
	<222> (1)..(9)	
	<400> 24	
	Met Leu Leu Pro Phe Thr Phe Val Leu	
	1 5	

<210> 25
 <211> 3150
 <212> DNA
 <213> Chlamydia pneumoniae

<220>
 <221> CDS
 10 <222> (100)..(3033)

<400> 25
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attacgattt taaaccttat ttaacgacag ggttgaggc atg cct ctt tct ttc	114
Met Pro Leu Ser Phe	
1	5

20 aaa tct tca tct ttt tgt cta ctt gcc tgt tta tgt agt gca agt tgc 162
 Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu Cys Ser Ala Ser Cys
 10 15 20

gcg ttt gct gag act aga ctc gga ggg aac ttt gtt cct cca att acg 210
 Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe Val Pro Pro Ile Thr
 25 30 35

aat cag ggt gaa gag atc tta ctc act tca gat ttt gtt tgt tca aac 258
 Asn Gln Gly Glu Ile Leu Leu Thr Ser Asp Phe Val Cys Ser Asn
 40 45 50

30 ttc ttg ggg gcg agt ttt tca agt tcc ttt atc aat agt tcc agc aat 306
 Phe Leu Gly Ala Ser Phe Ser Ser Phe Ile Asn Ser Ser Ser Asn
 55 60 65

ctc tcc tta tta ggg aag ggc ctt tcc tta acg ttt acc tct tgt caa 354
 Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr Phe Thr Ser Cys Gln
 70 75 80 85

40 gct cct aca aat agt aac tat gcg cta ctt tct gcc gca gag act ctg 402
 Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser Ala Ala Glu Thr Leu
 90 95 100

acc ttc aag aat ttt tct tct ata aac ttt aca ggg aac caa tcg aca 450
 Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr Gly Asn Gln Ser Thr
 105 110 115

gga ctt ggc ggc ctc atc tac gga aaa gat att gtt ttc caa tct atc 498
 Gly Leu Gly Leu Ile Tyr Gly Lys Asp Ile Val Phe Gln Ser Ile
 120 125 130

50 aaa gat ttg atc ttc act acg aac cgt gtt gcc tat tct cca gca tct 546
 Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala Tyr Ser Pro Ala Ser
 135 140 145

gta act acg tcg gca act ccc gca atc act aca gta act aca gga gcc 594
 Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr Val Thr Thr Gly Ala
 150 155 160 165

60 tct gct ctc caa cct aca gac tca ctc act gtc gaa aac ata tcc caa 642
 Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val Glu Asn Ile Ser Gln
 170 175 180

40/83

	tcg atc aag ttt ttt ggg aac ctt gcc aac ttc ggc tct gca att agc Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe Gly Ser Ala Ile Ser 185 190 195	690
	agt tct ccc acg gca gtc gtt aaa ttc atc aat aac acc gct acc atg Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn Asn Thr Ala Thr Met 200 205 210	738
10	agc ttc tcc cat aac ttt act tcg tca gga ggc ggc gtg att tat gga Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly Gly Val Ile Tyr Gly 215 220 225	786
	gga agc tct ctc ctt ttt gaa aac aat tct gga tgc atc atc ttc acc Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly Cys Ile Ile Phe Thr 230 235 240 245	834
20	gcc aac tcc tgt gtg aac agc tta aaa ggc gtc acc cct tca tca gga Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val Thr Pro Ser Ser Gly 250 255 260	882
	acc tat gct tta gga agt ggc gga gcc atc tgc atc cct acg gga act Thr Tyr Ala Leu Gly Ser Gly Ala Ile Cys Ile Pro Thr Gly Thr 265 270 275	930
	ttc gaa tta aaa aac aat cag ggg aag tgc acc ttc tct tat aat ggt Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr Phe Ser Tyr Asn Gly 280 285 290	978
30	aca cca aat gat gcg ggt gcg atc tac gcc gaa acc tgc aac atc gta Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu Thr Cys Asn Ile Val 295 300 305	1026
	ggg aac cag ggt gcc ttg ctc cta gat agc aac act gca gcg aga aat Gly Asn Gln Gly Ala Leu Leu Asp Ser Asn Thr Ala Ala Arg Asn 310 315 320 325	1074
40	ggc gga gcc atc tgt gct aaa gtg ctc aat att caa gga cgc ggt cct Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile Gln Gly Arg Gly Pro 330 335 340	1122
	att gaa ttc tct aga aac cgc gcg gag aag ggt gga gct att ttc ata Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly Gly Ala Ile Phe Ile 345 350 355	1170
	ggc ccc tct gtt gga gac cct gcg aag caa aca tcg aca ctt acg att Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr Ser Thr Leu Thr Ile 360 365 370	1218
50	ttg gct tcc gaa ggt gat att gcg ttc caa gga aac atg ctc aat aca Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly Asn Met Leu Asn Thr 375 380 385	1266
	aaa cct gga atc cgc aat gcc atc act gta gaa gca ggg gga gag att Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu Ala Gly Gly Glu Ile 390 395 400 405	1314
60	gtg tct cta tct gca caa gga ggc tca cgt ctt gta ttt tat gat ccc Val Ser Leu Ser Ala Gln Gly Ser Arg Leu Val Phe Tyr Asp Pro 410 415 420	1362

41/83

	att aca cat agc ctc cca acc aca agt ccg tct aat aaa gac att aca Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser Asn Lys Asp Ile Thr 425 430 435	1410
	atc aac gct aat ggc gct tca gga tct gta gtc ttt aca agt aag gga Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val Phe Thr Ser Lys Gly 440 445 450	1458
10	ctc tcc tct aca gaa ctc ctg ttg cct gcc aac acg aca act ata ctt Leu Ser Ser Thr Glu Leu Leu Pro Ala Asn Thr Thr Ile Leu 455 460 465	1506
	cta gga aca gtc aag atc gct agt gga gaa ctg aag att act gac aat Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu Lys Ile Thr Asp Asn 470 475 480 485	1554
20	gcg gtt gtc aat gtt gct ggc ttc gct act cag ggc tca ggt cag ctt Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln Gly Ser Gly Gln Leu 490 495 500	1602
	acc ctg ggc tct gga gga acc tta ggg ctg gca aca ccc acg gga gca Thr Leu Gly Ser Gly Thr Leu Gly Leu Ala Thr Pro Thr Gly Ala 505 510 515	1650
	cct gcc gct gta gac ttt acg att gga aag tta gca ttc gat cct ttt Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu Ala Phe Asp Pro Phe 520 525 530	1698
30	tcc ttc cta aaa aga gat ttt gtt tca gca tca gta aat gca ggc aca Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser Val Asn Ala Gly Thr 535 540 545	1746
	aaa aac gtc act tta aca gga gct ctg gtt ctt gat gaa cat gac gtt Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu Asp Glu His Asp Val 550 555 560 565	1794
40	aca gat ctt tat gat atg gtg tca tta caa tct cca gta gca att cct Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser Pro Val Ala Ile Pro 570 575 580	1842
	atc gct gtt ttc aaa gga gca acc gtt act aag aca gga ttt cct gat Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys Thr Gly Phe Pro Asp 585 590 595	1890
	ggg gag att gcg act cca agc cac tac ggc tac caa gga aag tgg tcc Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr Gln Gly Lys Trp Ser 600 605 610	1938
50	tac aca tgg tcc cgt ccc ctg tta att cca gct cct gat gga gga ttt Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala Pro Asp Gly Gly Phe 615 620 625	1986
	cct gga ggt ccc tct cct agc gca aat act ctc tat gct gta tgg aat Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu Tyr Ala Val Trp Asn 630 635 640 645	2034
60	tca gac act ctc gtg cgt tct acc tat atc tta gat ccc gag cgt tac Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu Asp Pro Glu Arg Tyr 650 655 660	2082

42/83

	gga gaa att gtc agc aac agc tta tgg att tcc ttc tta gga aat cag Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser Phe Leu Gly Asn Gln 665 670 675	2130
	gca ttc tct gat att ctc caa gat gtt ctt ttg ata gat cat ccc ggg Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu Ile Asp His Pro Gly 680 685 690	2178
10	ttg tcc ata acc gcg aaa gct tta gga gcc tat gtc gaa cac aca cca Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr Val Glu His Thr Pro 695 700 705	2226
	aga caa gga cat gag ggc ttt tca ggt cgc tat gga ggc tac caa gct Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr Gly Tyr Gln Ala 710 715 720 725	2274
20	gcg cta tct atg aac tac acg gac cac act acg tta gga ctt tct ttc Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr Leu Gly Leu Ser Phe 730 735 740	2322
	ggg cag ctt tat gga aaa act aac gcc aac ccc tac gat tca cgt tgc Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro Tyr Asp Ser Arg Cys 745 750 755	2370
	tca gaa caa atg tat tta ctc tcg ttc ttt ggt caa ttc cct atc gtg Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly Gln Phe Pro Ile Val 760 765 770	2418
30	act caa aag agc gag gcc tta att tcc tgg aaa gca gct tat ggt tat Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys Ala Ala Tyr Gly Tyr 775 780 785	2466
	tcc aaa aat cac cta aat acc acc tac ctc aga cct gac aaa gct cca Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg Pro Asp Lys Ala Pro 790 795 800 805	2514
40	aaa tct caa ggg caa tgg cat aac aat agt tac tat gtt ctt att tct Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr Tyr Val Leu Ile Ser 810 815 820	2562
	gca gaa cat cct cta aac tgg tgt ctt ctt aca aga cct ctg gct Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu Thr Arg Pro Leu Ala 825 830 835	2610
	caa gct tgg gat ctt tca ggt ttt att tcc gca gaa ttc cta ggt ggt Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala Glu Phe Leu Gly Gly 840 845 850	2658
50	tgg caa agt aag ttc aca gaa act gga gat ctg caa cgt agc ttt agt Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu Gln Arg Ser Phe Ser 855 860 865	2706
	aga ggt aaa ggg tac aat gtt tcc cta ccg ata gga tgt tct tct caa Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile Gly Cys Ser Ser Gln 870 875 880 885	2754
60	tgg ttc aca cca ttt aag aag gct cct tct aca ctg acc atc aaa ctt Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr Leu Thr Ile Lys Leu 890 895 900	2802

43/83

gcc tac aag cct gat atc tat cgt gtc aac cct cac aat att gtg act Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro His Asn Ile Val Thr 905 910 915	2850
gtc gtc tca aac caa gag agc act tcg atc tca gga gca aat cta cgc Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser Gly Ala Asn Leu Arg 920 925 930	2898
10 cgc cac ggt ttg ttt gta caa atc cat gat gta gta gat ctc acc gag Arg His Gly Leu Phe Val Gln Ile His Asp Val Val Asp Leu Thr Glu 935 940 945	2946
gac act cag gcc ttt cta aac tat acc ttt gac ggg aaa aat gga ttt Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp Gly Lys Asn Gly Phe 950 955 960 965	2994
20 aca aac cac cga gtg tct aca gga cta aaa tcc aca ttt taaaactcta Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser Thr Phe 970 975	3043
agctctgctt agagtttctt gtagccccgg tcgtcttaga atcctctatc catcatcgaa 3103 gaacttagca atgaaggcca agatttcac tctatgagaa cccccccc 3150	
 <210> 26 <211> 9 <212> PRT 30 <213> Chlamydia pneumoniae	
 <220> <221> SITE <222> (936)..(944)	
 <400> 26 Gly Leu Phe Val Gln Ile His Asp Val 1 5	
 40 <210> 27 <211> 841 <212> PRT <213> Chlamydia pneumoniae	
 <400> 27 Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu 1 5 10 15	
 50 Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala 20 25 30	
Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Ser Phe Ser Ser Lys 35 40 45	
Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val 50 55 60	
60 Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys 65 70 75 80	

44/83

	Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly			
	85	90	95	
	Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala			
	100	105	110	
	Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe			
	115	120	125	
10	Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly			
	130	135	140	
	Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp			
	145	150	155	160
	Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile			
	165	170	175	
20	Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe			
	180	185	190	
	Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn			
	195	200	205	
	Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala			
	210	215	220	
30	Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly			
	225	230	235	240
	Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn			
	245	250	255	
	Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly			
	260	265	270	
	Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile			
	275	280	285	
40	Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp			
	290	295	300	
	Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr			
	305	310	315	320
	Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys			
	325	330	335	
50	Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys			
	340	345	350	
	Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly			
	355	360	365	
	Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser			
	370	375	380	
60	Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn			
	385	390	395	400

45/83

	Ile Asp Ser Leu Arg Asn Gly Lys Ile Lys Leu Ser Ala Ala Thr			
	405	410	415	
	Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser			
	420	425	430	
10	Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr			
	435	440	445	
	Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala			
	450	455	460	
	Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly			
	465	470	475	480
	Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser			
	485	490	495	
20	Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu			
	500	505	510	
	Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln			
	515	520	525	
	Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe			
	530	535	540	
30	Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn			
	545	550	555	560
	Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser			
	565	570	575	
	Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu			
	580	585	590	
40	Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr			
	595	600	605	
	Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val			
	610	615	620	
	Val Ser Ile Leu Leu Gly Glu Gly Leu Arg Glu Ile Leu Leu Pro			
	625	630	635	640
	Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr			
	645	650	655	
50	Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro			
	660	665	670	
	Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala			
	675	680	685	
	Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly			
	690	695	700	
60	Phe Phe Gln Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala			
	705	710	715	720

46/83

Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser
 725 730 735
 Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu
 740 745 750
 Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro
 10 755 760 765
 Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Leu Leu Ser Asn
 770 775 780
 Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly
 785 790 795 800
 Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu
 805 810 815
 20 Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn
 820 825 830
 Val Asp Ala Gly Ser Lys Ile Lys Phe
 835 840

 <210> 28
 <211> 841
 30 <212> PRT
 <213> Chlamydia pneumoniae

 <400> 28
 Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu
 1 5 10 15
 Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala
 20 25 30
 40 Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
 35 40 45
 Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
 50 55 60
 Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys
 65 70 75 80
 Phe Lys Asn Asp Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly
 50 85 90 95
 50 Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala
 100 105 110
 Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe
 115 120 125
 Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly
 130 135 140

47/83

Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp
 145 150 155 160
 Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile
 165 170 175
 Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe
 10 180 185 190
 Ile Gly Asn Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn
 195 200 205
 Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala
 210 215 220
 Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly
 225 230 235 240
 20 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn
 245 250 255
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly
 260 265 270
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile
 275 280 285
 30 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp
 290 295 300
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr
 305 310 315 320
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys
 325 330 335
 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys
 40 340 345 350
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly
 355 360 365
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser
 370 375 380
 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn
 385 390 395 400
 50 Ile Asp Ser Leu Arg Asn Gly Lys Ile Lys Leu Ser Ala Ala Thr
 405 410 415
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser
 420 425 430
 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr
 435 440 445
 60 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala
 450 455 460

48/83

Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly
 465 470 475 480

Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser
 485 490 495

Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu
 10 500 505 510

Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln
 515 520 525

Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe
 530 535 540

Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn
 545 550 555 560

20 Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser
 565 570 575

Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu
 580 585 590

Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr
 595 600 605

30 Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val
 610 615 620

Val Ser Ile Leu Leu Gly Glu Gly Leu Arg Glu Ile Leu Leu Pro
 625 630 635 640

Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr
 645 650 655

40 Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro
 660 665 670

Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala
 675 680 685

Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly
 690 695 700

Phe Phe Gln Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala
 705 710 715 720

50 Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser
 725 730 735

Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu
 740 745 750

Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro
 755 760 765

60 Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Leu Leu Ser Asn
 770 775 780

49/83

Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly
 785 790 795 800

Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu
 805 810 815

Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn
 10 820 825 830

Val Asp Ala Gly Ser Lys Ile Lys Phe
 835 840

<210> 29

<211> 245

<212> PRT

<213> Chlamydia pneumoniae

20

<400> 29

Met Pro Pro Leu Asn Ala Asp Asp Val Leu Pro Arg Asp His Leu Ser
 1 5 10 15

Asp Gly Ser Phe Ser Asp Thr Tyr Pro Asp Ile Thr Thr Gln Ala Ile
 20 25 30

30

Ile Leu Ile Phe Leu Ala Leu Ser Pro Phe Leu Val Met Leu Leu Thr
 35 40 45

Ser Tyr Leu Lys Ile Ile Ile Thr Leu Val Leu Leu Arg Asn Ala Leu
 50 55 60

Gly Val Gln Gln Thr Pro Pro Ser Gln Val Leu Asn Gly Ile Ala Leu
 65 70 75 80

Ile Leu Ser Ile Tyr Val Met Phe Pro Thr Gly Val Ala Met Tyr Lys
 85 90 95

40

Asp Ala Arg Lys Glu Ile Glu Ala Asn Thr Ile Pro Gln Ser Leu Phe
 100 105 110

Thr Ala Glu Gly Ala Glu Thr Val Phe Val Ala Leu Asn Lys Ser Lys
 115 120 125

Glu Pro Leu Arg Ser Phe Leu Ile Arg Asn Thr Pro Lys Ala Gln Ile
 130 135 140

50

Gln Ser Phe Tyr Lys Ile Ser Gln Lys Thr Phe Pro Ser Glu Ile Arg
 145 150 155 160

Ala His Leu Thr Ala Ser Asp Phe Val Ile Ile Ile Pro Ala Phe Ile
 165 170 175

Met Gly Gln Ile Lys Asn Ala Phe Glu Ile Gly Val Leu Ile Tyr Leu
 180 185 190

Pro Phe Phe Val Ile Asp Leu Val Thr Ala Asn Val Leu Val Ala Met
 195 200 205

60

50/83

Gln Met Met Met Leu Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu
 210 215 220
 Leu Leu Ile Val Met Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu
 225 230 235 240
 10 Met Ile Ser Phe Lys
 245
 <210> 30
 <211> 233
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 30
 20 Met Lys Phe Phe Ser Leu Ile Phe Lys Asp Asp Asp Val Ser Pro Asn
 1 5 10 15
 Lys Lys Val Leu Ser Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys
 20 25 30
 Glu Leu Leu Glu Lys Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu
 35 40 45
 Thr Glu Gln Lys Cys Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly
 50 55 60
 30 Phe Lys Glu Gly Ser Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu
 65 70 75 80
 Glu Glu Thr Lys Asn Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro
 85 90 95
 Leu Ala Ile Ala Ser Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu
 100 105 110
 40 His Pro Glu Thr Ile Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu
 115 120 125
 Thr Gln Asn Lys His Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro
 130 135 140
 Leu Val Glu Lys Ser Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala
 145 150 155 160
 50 Asp Ser Leu Ile Leu Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys
 165 170 175
 Ile Ile Glu Thr Glu Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln
 180 185 190
 Leu Asp Ala Leu Glu Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn
 195 200 205
 Pro Val Asp Glu Pro Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser
 210 215 220
 60

51/83

Leu Ser Asn Asp Gln Asp Lys Lys Glu
 225 230

<210> 31
 <211> 322

<212> PRT

10 <213> Chlamydia pneumoniae

<400> 31

Met Thr Leu Leu Cys Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val
 1 5 10 15

His Gly Leu Pro Gly Arg Glu Ala Asn Glu Ile Val Val Leu Leu Val
 20 25 30

Ser Lys Gly Val Ala Ala Gln Lys Leu Pro Gln Ala Ala Ala Ala Thr
 20 35 40 45

Ala Gly Ala Ala Thr Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala
 50 55 60

Gln Ile Thr Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg
 65 70 75 80

Met Lys Gly Thr Ser Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val
 85 90 95

30 Pro Ser Glu Leu Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu
 100 105 110

Gln Met Ala Ser Thr Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser
 115 120 125

Val Gln Ile Ser Phe Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr
 130 135 140

40 Ala Ser Val Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser
 145 150 155 160

Ile Met Val Ser Lys Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly
 165 170 175

Leu Val Pro Glu Asn Val Ser Val Val Ser Asp Arg Ala Ala Tyr Ser
 180 185 190

50 Asp Ile Thr Ile Asn Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr
 195 200 205

Val Ser Val Trp Gly Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe
 210 215 220

Arg Leu Ile Phe Tyr Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys
 225 230 235 240

Gly Leu Leu Trp Val Ile Trp Lys Thr His Thr Leu Ile Met Thr Met
 245 250 255

60

52/83

Gly Gly Thr Lys Gly Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala
 260 265 270
 Leu Glu Ala Lys Lys Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys
 275 280 285
 Glu Asp Ala Asp Ser Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp
 10 290 295 300
 Lys Asp Ser Ser Asp Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu
 305 310 315 320
 Gly Ala

 <210> 32
 <211> 226
 20 <212> PRT
 <213> Chlamydia pneumoniae

 <400> 32
 Met Thr Ile Arg Val Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys
 1 5 10 15
 Ile Leu Asp Gly Val Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu
 20 25 30
 30 Phe Val Gly Lys Ser Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu
 35 40 45
 Ala Gly Leu Val Gln Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu
 50 55 60
 Ala Pro Ala Leu Val Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr
 65 70 75 80
 Val Leu Gly Asn Cys Thr His Pro Gln Ile His Ile Lys Gly Arg Ser
 40 85 90 95
 Thr Glu Glu Ala Arg Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp
 100 105 110
 Ile Glu Glu Val Ala Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln
 115 120 125
 Lys Gln Arg Val Ala Ile Val Arg Ser Leu Cys Met Asp Lys His Thr
 130 135 140
 50 Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala
 145 150 155 160
 Ser Phe Arg His Leu Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val
 165 170 175
 Gly Leu Thr Thr His Asp Met Gln Phe Val His Ser Cys Leu Asp Arg
 180 185 190
 60 Ile Tyr Leu Ile Asp Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg
 195 200 205

53/83

Asp Gly Glu Leu Asp Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser
 210 215 220

Ala Gln
 225

10 <210> 33
 <211> 436
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 33
 Met Lys Arg Pro Phe Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser
 1 5 10 15
 Cys Ala Ser Leu Ser Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg
 20 20 25 30
 Gly Ala Thr Ala Ala Val Val His Ala Asp Ser Gly Lys Val Phe Tyr
 35 40 45
 Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile
 50 55 60
 Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr
 65 70 75 80
 30 Leu Ile Lys Val Lys Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala
 85 90 95
 Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp
 100 105 110
 Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp
 115 120 125
 40 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val
 130 135 140
 Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu
 145 150 155 160
 Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn
 165 170 175
 50 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Arg Asp
 180 185 190
 Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly
 195 200 205
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly
 210 215 220
 Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Pro Gly Ser Thr
 225 230 235 240

54/83

	Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr			
	245	250	255	
	Ala Gly Lys Asn Leu Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu			
	260	265	270	
10	Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln			
	275	280	285	
	Asp Val Ile Ala Leu Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg			
	290	295	300	
	Lys Glu Leu Val Pro Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn			
	305	310	315	320
	Leu Gly Lys Leu Ser Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe			
	325	330	335	
20	Tyr Ala Ser Glu Asp Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His			
	340	345	350	
	Ala Asp Ala Phe Pro Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val			
	355	360	365	
	Phe Tyr Asp Asp Glu Gly Lys Lys Ile Ser Ser Gln Pro Phe Tyr Ala			
	370	375	380	
30	Pro Cys Arg Phe Glu Arg Thr Ile Lys Pro Trp Lys Leu Tyr Met Lys			
	385	390	395	400
	Arg Val Phe Thr Ser Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu			
	405	410	415	
	Met Tyr Phe Arg Ile Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His			
	420	425	430	
	Tyr Ser Lys Ile			
40	435			
	<210> 34			
	<211> 245			
	<212> PRT			
	<213> Chlamydia pneumoniae			
	<400> 34			
50	Val Val His Ala Asp Ser Gly Lys Val Phe Tyr			
	1	5	10	
	Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile			
	15	20	25	
	Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr			
	30	35	40	
	Leu Ile Lys Val Lys Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala			
	45	50	55	

55/83

	Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp			
	60	65	70	75
	Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp			
	80	85	90	
	Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val			
10	95	100	105	
	Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu			
	110	115	120	
	Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn			
	125	130	135	
	Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp			
	140	145	150	155
20	Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly			
	160	165	170	
	Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly			
	175	180	185	
	Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Pro Gly Ser Thr			
	190	195	200	
30	Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr			
	205	210	215	
	Ala Gly Lys Asn Leu Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu			
	220	225	230	235
	Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro			
	240	245		
40	<210> 35			
	<211> 645			
	<212> PRT			
	<213> Chlamydia pneumoniae			
	<400> 35			
	Met Ala Ser Asn Pro Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu			
	1	5	10	15
	Ala Lys Gln Arg Gln Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr			
50	20	25	30	
	Ile Asn Glu Gly Gln Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly			
	35	40	45	
	Lys Ser Val Ser Ala His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro			
	50	55	60	
	Phe Ser Val Ser Gly Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr			
	65	70	75	80

56/83

	Ala Ser Arg Ser Ile Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met			
	85	90	95	
	Ile Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu			
	100	105	110	
10	Gln Gln Phe Arg Glu Ile Ile His Thr His Leu Ala Leu Thr Ala Glu			
	115	120	125	
	Val Ala Lys Glu Lys Met Leu Tyr Ala Leu Glu Glu Thr Phe His			
	130	135	140	
	Asp Pro Arg Leu Cys Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly			
	145	150	155	160
	Met Leu Gln Arg Ile Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys			
	165	170	175	
20	Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln			
	180	185	190	
	Tyr Gln Ile Leu Gln Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met			
	195	200	205	
	Ser Leu Leu Ile Ile Thr His Asn Met Gly Val Val Ala Glu Thr Ala			
	210	215	220	
30	Asp Asp Val Leu Val Leu Tyr Ala Gly Arg Met Val Glu Cys Ala Pro			
	225	230	235	240
	Ala Val Gln Met Phe His Asn Pro Ser His Pro Tyr Thr Arg Asp Leu			
	245	250	255	
	Leu Ala Ser Arg Pro Ser Leu Gln Pro Gln Gln Leu Gly Ser Phe Asn			
	260	265	270	
40	Pro Ile Pro Gly Gln Pro Pro His Tyr Thr Ala Phe Pro Ser Gly Cys			
	275	280	285	
	Arg Tyr His Pro Arg Cys Ser Lys Ile Leu Asn Arg Cys Ser Ala Glu			
	290	295	300	
	Ala Pro Glu Ile Tyr Pro Val Arg Glu Gly His Lys Val Arg Val Gly			
	305	310	315	320
	Cys Met Thr Thr Asn Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu			
	325	330	335	
50	Thr Lys His Tyr Tyr Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile			
	340	345	350	
	Ala Ser Arg Pro Val Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg			
	355	360	365	
	Ala Val Gly Leu Ile Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala			
	370	375	380	
60	Leu Ala Leu Ala Gly Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe			
	385	390	395	400

57/83

Asn Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu
 405 410 415

Arg Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn
 420 425 430

Pro Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His
 10 435 440 445

Lys Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu
 450 455 460

Glu Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln
 465 470 475 480

Leu Ser Gly Gly Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu
 485 490 495

20 Gly Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp
 500 505 510

Leu Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys
 515 520 525

Lys Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val
 530 535 540

30 Arg Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val
 545 550 555 560

Glu Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr
 565 570 575

Thr Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg
 580 585 590

40 Gln Ser Lys Pro Ile Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser
 595 600 605

Cys Ser Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu
 610 615 620

Ala Cys Lys Ser Glu Ile Ile Pro Asn Gln Gly Asp Ala His His Thr
 625 630 635 640

Tyr Arg Cys Ile His
 645

50 <210> 36
 <211> 588
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 36
 Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu
 1 5 10

Ala Lys Gln Arg Gln Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr
 15 20 25
 Ile Asn Glu Gly Gln Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly
 30 35 40
 10 Lys Ser Val Ser Ala His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro
 45 50 55
 Phe Ser Val Ser Gly Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr
 60 65 70 75
 Ala Ser Arg Ser Ile Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met
 80 85 90
 Ile Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu
 95 100 105
 20 Gln Gln Phe Arg Glu Ile Ile His Thr His Leu Ala Leu Thr Ala Glu
 110 115 120
 Val Ala Lys Glu Lys Met Leu Tyr Ala Leu Glu Glu Thr Gly Phe His
 125 130 135
 Asp Pro Arg Leu Cys Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly
 140 145 150 155
 30 Met Leu Gln Arg Ile Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys
 160 165 170
 Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln
 175 180 185
 Tyr Gln Ile Leu Gln Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met
 190 195 200
 40 Ser Leu Leu Ile Ile Thr His Asn Met Gly Val Val Ala Glu Thr Ala
 205 210 215
 Asp Asp Val Leu Val Leu Tyr Ala Gly Arg Met Val Glu Cys Ala Pro
 220 225 230 235
 Ala Val Gln Met Phe His Asn Pro Ser His Pro Tyr Thr Arg Asp Leu
 240 245 250
 Leu Ala Ser Arg Pro Ser Leu Gln Pro Gln Gln Leu Gly Ser Phe Asn
 255 260 265
 50 Pro Ile Pro Gly Gln Pro Pro His Tyr Thr Ala Phe Pro Ser Gly Cys
 270 275 280
 Arg Tyr His Pro Arg Cys Ser Lys Ile Leu Asn Arg Cys Ser Ala Glu
 285 290 295
 Ala Pro Glu Ile Tyr Pro Val Arg Glu Gly His Lys Val Arg Val Gly
 300 305 310 315
 60 Cys Met Thr Thr Asn Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu
 320 325 330

59/83

Thr Lys His Tyr Tyr Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile
 335 340 345
 Ala Ser Arg Pro Val Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg
 350 355 360
 Ala Val Gly Leu Ile Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala
 10 365 370 375
 Leu Ala Leu Ala Gly Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe
 380 385 390 395
 Asn Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu
 400 405 410
 Arg Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn
 415 420 425
 20 Pro Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His
 430 435 440
 Lys Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu
 445 450 455
 Glu Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln
 460 465 470 475
 30 Leu Ser Gly Gly Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu
 480 485 490
 Gly Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp
 495 500 505
 Leu Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys
 510 515 520
 Lys Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val
 40 525 530 535
 Arg Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val
 540 545 550 555
 Glu Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr
 560 565 570
 Thr Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg
 575 585
 50 Gln

 <210> 37
 <211> 698
 <212> PRT
 <213> Chlamydia pneumoniae .

<400> 37
 60 Met Pro Gly Ile Glu Lys Ala Ala Thr Thr Val Ala Val Pro Gln Asp
 1 5 10 15

60/83

	Lys Ser Glu Glu Glu Lys Val Lys Glu Arg Leu Thr Lys Arg Glu Leu			
	20	25	30	
	Thr Cys Glu Asp Leu Lys Asp Asn Gly Tyr Thr Val Asn Phe Glu Asp			
	35	40	45	
10	Ile Ser Ile Leu Glu Leu Leu Gln Phe Val Ser Lys Ile Ser Gly Thr			
	50	55	60	
	Asn Phe Val Phe Asp Ser Asn Asp Leu Gln Phe Asn Val Thr Ile Val			
	65	70	75	80
	Ser His Asp Pro Thr Ser Val Asp Asp Leu Ser Thr Ile Leu Leu Gln			
	85	90	95	
	Val Leu Lys Met His Asp Leu Lys Val Val Glu Gln Gly Asn Asn Val			
	100	105	110	
20	Leu Ile Tyr Arg Asn Pro His Leu Ser Lys Leu Ser Thr Val Val Thr			
	115	120	125	
	Asp Ser Ser Leu Lys Glu Thr Cys Glu Ala Val Val Val Thr Arg Val			
	130	135	140	
	Phe Arg Leu Tyr Arg Arg Gln Pro Ser Ala Ala Val Asn Ile Ile Gln			
	145	150	155	160
30	Pro Leu Leu Ser His Asp Ala Ile Val Ser Ala Ser Glu Ala Thr Arg			
	165	170	175	
	His Val Ile Ile Ser Asp Ile Ala Gly Asn Val Asp Lys Val Ser Asp			
	180	185	190	
	Leu Leu Ala Ala Leu Asp Cys Pro Gly Thr Ser Val Asp Met Thr Glu			
	195	200	205	
40	Tyr Glu Val Lys Tyr Ala Asn Pro Ala Ala Leu Val Ser Tyr Cys Gln			
	210	215	220	
	Asp Val Leu Gly Thr Leu Ala Glu Asp Asp Ala Phe Gln Met Phe Ile			
	225	230	235	240
	Gln Pro Gly Thr Asn Lys Ile Phe Val Val Ser Ser Pro Arg Leu Ala			
	245	250	255	
	Asn Lys Ala Glu Gln Leu Leu Lys Ser Leu Asp Val Pro Glu Met Ala			
	260	265	270	
50	His Thr Leu Asp Asp Pro Ala Ser Thr Ala Leu Ala Leu Gly Gly Thr			
	275	280	285	
	Gly Thr Thr Ser Pro Lys Ser Leu Arg Phe Phe Met Tyr Lys Leu Lys			
	290	295	300	
	Tyr Gln Asn Gly Glu Val Ile Ala Asn Ala Leu Gln Asp Ile Gly Tyr			
	305	310	315	320
60	Asn Leu Tyr Val Thr Thr Ala Met Asp Glu Asp Phe Ile Asn Thr Leu			
	325	330	335	

	Asn Ser Ile Gln Trp Leu Glu Val Asn Asn Ser Ile Val Ile Ile Gly			
	340	345	350	
	Asn Gln Gly Asn Val Asp Arg Val Ile Gly Leu Leu Asn Gly Leu Asp			
	355	360	365	
10	Leu Pro Pro Lys Gln Val Tyr Ile Glu Val Leu Ile Leu Asp Thr Ser			
	370	375	380	
	Leu Glu Lys Ser Trp Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp			
	385	390	395	400
	Glu Gln Ser Lys Val Ala Tyr Ala Ser Gly Leu Leu Asn Asn Thr Gly			
	405	410	415	
	Ile Ala Thr Pro Thr Lys Ala Thr Val Pro Pro Gly Thr Pro Asn Pro			
	420	425	430	
20	Gly Ser Ile Pro Leu Pro Thr Pro Gly Gln Leu Thr Gly Phe Ser Asp			
	435	440	445	
	Met Leu Asn Ser Ser Ala Phe Gly Leu Gly Ile Ile Gly Asn Val			
	450	455	460	
	Leu Ser His Lys Gly Lys Ser Phe Leu Thr Leu Gly Gly Leu Leu Ser			
	465	470	475	480
30	Ala Leu Asp Gln Asp Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile			
	485	490	495	
	Met Ala Gln Asp Thr Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val			
	500	505	510	
	Pro Tyr Gln Thr Ile Lys Tyr Tyr Ile Gln Glu Thr Gly Thr Val Thr			
	515	520	525	
40	Gln Asn Ile Asp Tyr Glu Asp Ile Gly Val Asn Leu Val Val Thr Ser			
	530	535	540	
	Thr Val Ala Pro Asn Asn Val Val Thr Leu Gln Ile Glu Gln Thr Ile			
	545	550	555	560
	Ser Glu Leu His Ser Ala Ser Gly Ser Leu Thr Pro Val Thr Asp Lys			
	565	570	575	
	Thr Tyr Ala Ala Thr Arg Leu Gln Ile Pro Asp Gly Cys Phe Leu Val			
	580	585	590	
50	Met Ser Gly His Ile Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val			
	595	600	605	
	Pro Leu Leu Asn Ser Ile Pro Leu Ile Arg Gly Leu Phe Ser Arg Thr			
	610	615	620	
	Ile Asp Gln Arg Gln Lys Arg Asn Ile Met Met Phe Ile Lys Pro Lys			
	625	630	635	640
60	Val Ile Ser Ser Phe Glu Glu Gly Thr Arg Val Thr Asn Lys Glu Gly			
	645	650	655	

62/83

Tyr Arg Tyr Asn Trp Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro
 660 665 670

Arg His Ala Pro Glu Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser
 675 680 685

Asp Phe Lys Ile Ile Glu Ile Glu Ala Gln
 10 690 695

<210> 38

<211> 547

<212> PRT

<213> Chlamydia pneumoniae

<400> 38

Met Ser Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn
 20 1 5 10 15

Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu
 20 25 30

Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe
 35 40 45

Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly
 50 55 60

30 Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala
 65 70 75 80

Gln Ser Leu Asp Arg Ala Ala Phe Phe Arg Arg Phe Ser Arg Leu
 85 90 95

Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu
 100 105 110

40 Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu
 115 120 125

Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn
 130 135 140

Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly
 145 150 155 160

50 Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala
 165 170 175

Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala
 180 185 190

Leu Val Ile Gly Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val
 195 200 205

Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser
 210 215 220

63/83

	Val Arg Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser			
	225	230	235	240
	Ile Phe Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val			
	245	250	255	
	His Glu Ile Gly Pro Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln			
10	260	265	270	
	Leu Pro Ile His Leu Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro			
	275	280	285	
	Ala Ile Ser Arg Cys Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys			
	290	295	300	
	Leu Met Lys Phe Val Leu Thr Leu Thr Met Ser Val Met Ile Ile Met			
	305	310	315	320
20	Thr Ala Gly Leu Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr			
	325	330	335	
	Glu His Gly Leu Phe Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val			
	340	345	350	
	Leu Arg Gly Tyr Gly Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu			
	355	360	365	
30	Val Ser Val Leu Phe Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe			
	370	375	380	
	Ile Gly Ile Gly Thr Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu			
	385	390	395	400
	Gly Arg Trp Val Leu Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser			
	405	410	415	
	Ile Thr Ala Trp Val Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys			
40	420	425	430	
	Arg Leu Pro Met Tyr Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser			
	435	440	445	
	Ile Lys Val Met Gly Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly			
	450	455	460	
	Leu Asn Ile Leu Thr Gln Thr Tyr Val Ile Phe Leu Asn Pro Leu			
	465	470	475	480
50	Thr Pro Leu Ala Trp Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala			
	485	490	495	
	Phe Leu Ser Glu Ser Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala			
	500	505	510	
	Lys Leu Leu Arg Val Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr			
	515	520	525	
60	Trp Arg Gly Gln Arg Gly Leu Leu Gln Arg Gln His Val Met Gln Asp			
	530	535	540	

64/83

Thr Gln Asn
545

<210> 39
<211> 535
<212> PRT

10 <213> Chlamydia pneumoniae

<400> 39

Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn
1 5 10

Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu
15 20 25 30

Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe
20 35 40 45

Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly
50 55 60

Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala
65 70 75

Gln Ser Leu Asp Arg Ala Ala Phe Phe Arg Arg Phe Ser Arg Leu
80 85 90

30 Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu
95 100 105 110

Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu
115 120 125

Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn
130 135 140

40 Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly
145 150 155

Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala
160 165 170

Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala
175 180 185 190

50 Leu Val Ile Gly Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val
195 200 205

Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser
210 215 220

Val Arg Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser
225 230 235

Ile Phe Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val
240 245 250

60

65/83

	His	Glu	Ile	Gly	Pro	Leu	Tyr	Leu	Met	Tyr	Ser	Leu	Lys	Ile	Tyr	Gln	
	255				260				265				270				
	Leu	Pro	Ile	His	Leu	Phe	Gly	Phe	Gly	Val	Phe	Thr	Val	Leu	Leu	Pro	
					275				280				285				
10	Ala	Ile	Ser	Arg	Cys	Val	Gln	Arg	Glu	Asp	His	Glu	Arg	Gly	Leu	Lys	
					290			295					300				
	Leu	Met	Lys	Phe	Val	Leu	Thr	Leu	Thr	Met	Ser	Val	Met	Ile	Ile	Met	
					305			310					315				
	Thr	Ala	Gly	Leu	Leu	Leu	Ala	Leu	Pro	Gly	Val	Arg	Val	Leu	Tyr		
					320			325				330					
20	Glu	His	Gly	Leu	Phe	Pro	Gln	Ser	Ala	Val	Tyr	Ala	Ile	Val	Arg	Val	
	335				340				345				350				
	Leu	Arg	Gly	Tyr	Gly	Ala	Ser	Ile	Ile	Pro	Met	Ala	Leu	Ala	Pro	Leu	
					355			360				365					
	Val	Ser	Val	Leu	Phe	Tyr	Ala	Gln	Arg	Gln	Tyr	Ala	Val	Pro	Leu	Phe	
					370			375				380					
	Ile	Gly	Ile	Gly	Thr	Ala	Leu	Ala	Asn	Ile	Val	Leu	Ser	Leu	Val	Leu	
					385			390				395					
30	Gly	Arg	Trp	Val	Leu	Lys	Asp	Val	Ser	Gly	Ile	Ser	Tyr	Ala	Thr	Ser	
					400			405				410					
	Ile	Thr	Ala	Trp	Val	Gln	Leu	Tyr	Phe	Leu	Trp	Tyr	Tyr	Ser	Ser	Lys	
					415			420			425				430		
	Arg	Leu	Pro	Met	Tyr	Ser	Lys	Leu	Leu	Trp	Glu	Ser	Ile	Arg	Arg	Ser	
					435			440			445						
40	Ile	Lys	Val	Met	Gly	Thr	Thr	Met	Leu	Ala	Cys	Met	Ile	Thr	Leu	Gly	
					450			455				460					
	Leu	Asn	Ile	Leu	Thr	Gln	Thr	Thr	Tyr	Val	Ile	Phe	Leu	Asn	Pro	Leu	
					465			470				475					
	Thr	Pro	Leu	Ala	Trp	Pro	Leu	Ser	Ser	Ile	Thr	Ala	Gln	Ala	Ile	Ala	
					480			485				490					
	Phe	Leu	Ser	Glu	Ser	Cys	Ile	Phe	Leu	Ala	Phe	Leu	Phe	Gly	Phe	Ala	
					495			500			505				510		
50	Lys	Leu	Leu	Arg	Val	Glu	Asp	Leu	Ile	Asn	Leu	Ala	Ser	Phe	Glu	Tyr	
					515			520				525					
	Trp	Arg	Gly	Gln	Arg	Gly	Leu	Leu	Gln								
					530			535									

<210> 40
 <211> 954
 <212> PRT
 <213> Chlamydia pneumoniae

66/83

<400> 40

Met	Lys	Thr	Ser	Arg	Asn	Lys	Gln	Cys	Lys	Ile	Thr	Asp	Pro	Leu	Ser
1															15

Lys	Ser	Ser	Phe	Phe	Val	Gly	Ala	Leu	Leu	Gly	Lys	Thr	Thr	Ile
														30
20								25						

10	Leu	Leu	Asn	Ala	Thr	Pro	Leu	Ser	Asp	Tyr	Phe	Asp	Asn	Gln	Ala	Asn
															45	
							35	40								

Gln	Leu	Thr	Thr	Leu	Phe	Pro	Leu	Ile	Asp	Thr	Leu	Thr	Asn	Met	Thr
															60
50								55							

Pro	Tyr	Ser	His	Arg	Ala	Thr	Leu	Phe	Gly	Val	Arg	Asp	Asp	Thr	Asn
															80
65								70			75				

20	Gln	Asp	Ile	Val	Leu	Asp	His	Gln	Asn	Ser	Ile	Glu	Ser	Trp	Phe	Glu
															95	
								85	90							

Asn	Phe	Ser	Gln	Asp	Gly	Gly	Ala	Leu	Ser	Cys	Lys	Ser	Leu	Ala	Ile
															110
100								105							

Thr	Asn	Thr	Lys	Asn	Gln	Ile	Leu	Phe	Leu	Asn	Ser	Phe	Ala	Ile	Lys
															125
115								120							

Arg	Ala	Gly	Ala	Met	Tyr	Val	Asp	Gly	Asn	Phe	Asp	Leu	Ser	Glu	Asn
															140
130								135							

30	His	Gly	Ser	Ile	Ile	Phe	Ser	Gly	Asn	Leu	Ser	Phe	Pro	Asn	Ala	Ser
															160	
145							150				155					

Asn	Phe	Ala	Asp	Thr	Cys	Thr	Gly	Gly	Ala	Val	Leu	Cys	Ser	Lys	Asn
															175
165								170							

Val	Thr	Ile	Ser	Lys	Asn	Gln	Gly	Thr	Ala	Tyr	Phe	Ile	Asn	Asn	Lys
															190
180								185							

40	Ala	Lys	Ser	Ser	Gly	Gly	Ala	Ile	Gln	Ala	Ala	Ile	Ile	Asn	Ile	Lys
															205	
								195		200						

Asp	Asn	Thr	Gly	Pro	Cys	Leu	Phe	Phe	Asn	Asn	Ala	Ala	Gly	Gly	Thr
								210	215						220

Ala	Gly	Gly	Ala	Leu	Phe	Ala	Asn	Ala	Cys	Arg	Ile	Glu	Asn	Asn	Ser
															240
225								230			235				

50	Gln	Pro	Ile	Tyr	Phe	Leu	Asn	Asn	Gln	Ser	Gly	Leu	Gly	Gly	Ala	Ile
															255	
								245		250						

Arg	Val	His	Gln	Glu	Cys	Ile	Leu	Thr	Lys	Asn	Thr	Gly	Ser	Val	Ile
															270
260								265							

Phe	Asn	Asn	Asn	Phe	Ala	Met	Glu	Ala	Asp	Ile	Ser	Ala	Asn	His	Ser
															285
275								280							

Ser	Gly	Gly	Ala	Ile	Tyr	Cys	Ile	Ser	Cys	Ser	Ile	Lys	Asp	Asn	Pro
															300
290								295							

67/83

	Gly Ile Ala Ala Phe Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala	
	305 310 315 320	
	Ile Cys Thr Gln Ser Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe	
	325 330 335	
10	Thr Asn Asn Gln Gly Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp	
	340 345 350	
	Gly Ala Cys Thr Leu Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn	
	355 360 365	
	Asn Arg His Phe Lys Asp Thr Phe Ser Asn His Val Ser Val Asn Cys	
	370 375 380	
20	Thr Arg Asn Val Ser Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala	
	385 390 395 400	
	Thr Phe Tyr Asp Pro Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile	
	405 410 415	
	Gln Lys Phe Asn Pro Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser	
	420 425 430	
	Ser Thr Tyr Ile Pro Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser	
	435 440 445	
30	His Phe Arg Asn His Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu	
	450 455 460	
	Asp Arg Ala Glu Trp Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr	
	465 470 475 480	
	Leu Arg Leu Gly Ser Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln	
	485 490 495	
40	Ser Ser Ser Ser Val Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile	
	500 505 510	
	Asn Leu Pro Ser Ile Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile	
	515 520 525	
	Arg Pro Thr Gly Ser Ser Ala Pro Tyr Ser Glu Asp Asn Asn Pro Ile	
	530 535 540	
	Ile Asn Leu Ser Gly Pro Leu Ser Leu Leu Asp Asp Glu Asn Leu Asp	
	545 550 555 560	
50	Pro Tyr Asp Thr Ala Asp Leu Ala Gln Pro Ile Ala Glu Val Pro Leu	
	565 570 575	
	Leu Tyr Leu Leu Asp Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe	
	580 585 590	
	Tyr Pro Glu Gly Leu Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val	
	595 600 605	
60	Trp Ser Pro Tyr Trp Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser	
	610 615 620	

68/83

Glu Asp Thr Val Asn Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr
 625 630 635 640

Pro Thr Gly Tyr Lys Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu
 645 650 655

Ser Ala Phe Trp Gln Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr
 10 660 665 670

Gln Thr Gln Gln Gly Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr
 675 680 685

Arg Leu Phe Val His Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His
 690 695 700

Met Glu Ala Thr Gly Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser
 705 710 715 720

20 Asn His Ser Phe Gly Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr
 725 730 735

Glu Ser His Ser Asp Asn Ser Val Ala Ser His Thr Thr Thr Val Ala
 740 745 750

Leu Gln Ile Asn Asn Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala
 755 760 765

30 Ser Leu Ala Tyr Ser Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr
 770 775 780

Ser Gly Lys Ile Gln Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly
 785 790 795 800

Ala Ala Leu Ser Cys Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro Leu
 805 810 815

40 His Phe Thr Pro Phe Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr
 820 825 830

Ala Phe Gln Glu Ser Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys
 835 840 845

Pro Leu Tyr Asn Leu Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu
 850 855 860

Ser Lys Phe Arg Leu Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln
 865 870 875 880

50 Pro Val Leu Tyr Gln Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser
 885 890 895

Ser Gly Ser Ser Trp Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala
 900 905 910

Ile Ala Phe Lys Gly Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser
 915 920 925

60 Val Phe Leu Asp Tyr Gln Gly Ser Val Ser Ser Thr Thr Thr His
 930 935 940

69/83

Tyr Leu His Ala Gly Thr Thr Phe Lys Phe
 945 950

<210> 41
 <211> 788

<212> PRT

10 <213> Chlamydia pneumoniae

<400> 41
 Thr Gly Gly Ala Val Leu Cys Ser Lys Asn
 1 5 10

Val Thr Ile Ser Lys Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys
 15 20 25

Ala Lys Ser Ser Gly Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys
 20 30 35 40

Asp Asn Thr Gly Pro Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr
 45 50 55

Ala Gly Gly Ala Leu Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser
 60 65 70

Gln Pro Ile Tyr Phe Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile
 75 80 85 90

30 Arg Val His Gln Glu Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile
 95 100 105

Phe Asn Asn Asn Phe Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser
 110 115 120

Ser Gly Gly Ala Ile Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro
 125 130 135

40 Gly Ile Ala Ala Phe Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala
 140 145 150

Ile Cys Thr Gln Ser Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe
 155 160 165 170

Thr Asn Asn Gln Gly Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp
 175 180 185

50 Gly Ala Cys Thr Leu Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn
 190 195 200

Asn Arg His Phe Lys Asp Thr Phe Ser Asn His Val Ser Val Asn Cys
 205 210 215

Thr Arg Asn Val Ser Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala
 220 225 230

Thr Phe Tyr Asp Pro Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile
 235 240 245 250

60

70/83

Gln Lys Phe Asn Pro Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser
 255 260 265
 Ser Thr Tyr Ile Pro Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser
 270 275 280
 His Phe Arg Asn His Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu
 10 285 290 295
 Asp Arg Ala Glu Trp Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr
 300 305 310
 Leu Arg Leu Gly Ser Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln
 315 320 325 330
 Ser Ser Ser Val Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile
 335 340 345
 20 Asn Leu Pro Ser Ile Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile
 350 355 360
 Arg Pro Thr Gly Ser Ser Ala Pro Tyr Ser Glu Asp Asn Asn Pro Ile
 365 370 375
 Ile Asn Leu Ser Gly Pro Leu Ser Leu Leu Asp Asp Glu Asn Leu Asp
 380 385 390
 30 Pro Tyr Asp Thr Ala Asp Leu Ala Gln Pro Ile Ala Glu Val Pro Leu
 395 400 405 410
 Leu Tyr Leu Leu Asp Val Thr Ala Lys His Ile Asn Thr Asp Asn Phe
 415 420 425
 Tyr Pro Glu Gly Leu Asn Thr Thr Gln His Tyr Gly Tyr Gln Gly Val
 430 435 440
 Trp Ser Pro Tyr Trp Ile Glu Thr Ile Thr Thr Ser Asp Thr Ser Ser
 40 445 450 455
 Glu Asp Thr Val Asn Thr Leu His Arg Gln Leu Tyr Gly Asp Trp Thr
 460 465 470
 Pro Thr Gly Tyr Lys Val Asn Pro Glu Asn Lys Gly Asp Ile Ala Leu
 475 480 485 490
 Ser Ala Phe Trp Gln Ser Phe His Asn Leu Phe Ala Thr Leu Arg Tyr
 495 500 505
 50 Gln Thr Gln Gln Gly Gln Ile Ala Pro Thr Ala Ser Gly Glu Ala Thr
 510 515 520
 Arg Leu Phe Val His Gln Asn Ser Asn Asn Asp Ala Lys Gly Phe His
 525 530 535
 Met Glu Ala Thr Gly Tyr Ser Leu Gly Thr Thr Ser Asn Thr Ala Ser
 540 545 550
 60 Asn His Ser Phe Gly Val Asn Phe Ser Gln Leu Phe Ser Asn Leu Tyr
 555 560 565 570

71/83

Glu Ser His Ser Asp Asn Ser Val Ala Ser His Thr Thr Thr Val Ala
 575 580 585
 Leu Gln Ile Asn Asn Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala
 590 595 600
 Ser Leu Ala Tyr Ser Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr
 10 605 610 615
 Ser Gly Lys Ile Gln Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly
 620 625 630
 Ala Ala Leu Ser Cys Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro Leu
 635 640 645 650
 His Phe Thr Pro Phe Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr
 655 660 665
 20 Ala Phe Gln Glu Ser Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys
 670 675 680
 Pro Leu Tyr Asn Leu Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu
 685 690 695
 Ser Lys Phe Arg Leu Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln
 700 705 710
 30 Pro Val Leu Tyr Gln Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser
 715 720 725 730
 Ser Gly Ser Ser Trp Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala
 735 740 745
 Ile Ala Phe Lys Gly Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser
 750 755 760
 Val Phe Leu Asp Tyr Gln Gly Ser Val Ser Ser Thr Thr Thr His
 40 765 770 775
 Tyr Leu His Ala Gly Thr Thr Phe Lys Phe
 780 785

<210> 42
 <211> 1000
 <212> PRT
 <213> Chlamydia pneumoniae
 50 <400> 42
 Met Gln Val Phe Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp
 1 5 10 15
 Ile Ser Ser Ser Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg Met
 20 25 30
 Arg Phe Leu Thr Ile Ser Asp Gln Asn Arg Lys Ile Lys Glu Pro Leu
 35 40 45

60

72/83

	Val Ser Lys Thr Pro Pro Lys Phe Leu Phe Tyr Leu Gly Asn Phe Thr			
50	55	60		
	Ala Cys Met Phe Gly Met Thr Pro Ala Val Tyr Ser Leu Gln Thr Asp			
65	70	75	80	
10	Ser Leu Glu Lys Phe Ala Leu Glu Arg Asp Glu Glu Phe Arg Thr Ser			
	85	90	95	
	Phe Pro Leu Leu Asp Ser Leu Ser Thr Leu Thr Gly Phe Ser Pro Ile			
	100	105	110	
	Thr Thr Phe Val Gly Asn Arg His Asn Ser Ser Gln Asp Ile Val Leu			
	115	120	125	
20	Ser Asn Tyr Lys Ser Ile Asp Asn Ile Leu Leu Leu Trp Thr Ser Ala			
	130	135	140	
	Gly Gly Ala Val Ser Cys Asn Asn Phe Leu Leu Ser Asn Val Glu Asp			
	145	150	155	160
	His Ala Phe Phe Ser Lys Asn Leu Ala Ile Gly Thr Gly Gly Ala Ile			
	165	170	175	
	Ala Cys Gln Gly Ala Cys Thr Ile Thr Lys Asn Arg Gly Pro Leu Ile			
	180	185	190	
30	Phe Phe Ser Asn Arg Gly Leu Asn Asn Ala Ser Thr Gly Gly Glu Thr			
	195	200	205	
	Arg Gly Gly Ala Ile Ala Cys Asn Gly Asp Phe Thr Ile Ser Gln Asn			
	210	215	220	
	Gln Gly Thr Phe Tyr Phe Val Asn Asn Ser Val Asn Asn Trp Gly Gly			
	225	230	235	240
40	Ala Leu Ser Thr Asn Gly His Cys Arg Ile Gln Ser Asn Arg Ala Pro			
	245	250	255	
	Leu Leu Phe Phe Asn Asn Thr Ala Pro Ser Gly Gly Ala Leu Arg			
	260	265	270	
	Ser Glu Asn Thr Thr Ile Ser Asp Asn Thr Arg Pro Ile Tyr Phe Lys			
	275	280	285	
50	Asn Asn Cys Gly Asn Asn Gly Gly Ala Ile Gln Thr Ser Val Thr Val			
	290	295	300	
	Ala Ile Lys Asn Asn Ser Gly Ser Val Ile Phe Asn Asn Asn Thr Ala			
	305	310	315	320
	Leu Ser Gly Ser Ile Asn Ser Gly Asn Gly Ser Gly Gly Ala Ile Tyr			
	325	330	335	
	Thr Thr Asn Leu Ser Ile Asp Asp Asn Pro Gly Thr Ile Leu Phe Asn			
	340	345	350	
60	Asn Asn Tyr Cys Ile Arg Asp Gly Gly Ala Ile Cys Thr Gln Phe Leu			
	355	360	365	

73/83

Thr Ile Lys Asn Ser Gly His Val Tyr Phe Thr Asn Asn Gln Gly Asn
 370 375 380
 Trp Gly Gly Ala Leu Met Leu Leu Gln Asp Ser Thr Cys Leu Leu Phe
 385 390 395 400
 Ala Glu Gln Gly Asn Ile Ala Phe Gln Asn Asn Glu Val Phe Leu Thr
 10 405 410 415
 Thr Phe Gly Arg Tyr Asn Ala Ile His Cys Thr Pro Asn Ser Asn Leu
 420 425 430
 Gln Leu Gly Ala Asn Lys Gly Tyr Thr Thr Ala Phe Phe Asp Pro Ile
 435 440 445
 Glu His Gln His Pro Thr Thr Asn Pro Leu Ile Phe Asn Pro Asn Ala
 450 455 460
 20 Asn His Gln Gly Thr Ile Leu Phe Ser Ser Ala Tyr Ile Pro Glu Ala
 465 470 475 480
 Ser Asp Tyr Glu Asn Asn Phe Ile Ser Ser Ser Lys Asn Thr Ser Glu
 485 490 495
 Leu Arg Asn Gly Val Leu Ser Ile Glu Asp Arg Ala Gly Trp Gln Phe
 500 505 510
 30 Tyr Lys Phe Thr Gln Lys Gly Ile Leu Lys Leu Gly His Ala Ala
 515 520 525
 Ser Ile Ala Thr Thr Ala Asn Ser Glu Thr Pro Ser Thr Ser Val Gly
 530 535 540
 Ser Gln Val Ile Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile Leu
 545 550 555 560
 Ala Lys Gly Lys Ala Pro Thr Leu Trp Ile Arg Pro Leu Gln Ser Ser
 40 565 570 575
 Ala Pro Phe Thr Glu Asp Asn Asn Pro Thr Ile Thr Leu Ser Gly Pro
 580 585 590
 Leu Thr Leu Leu Asn Glu Glu Asn Arg Asp Pro Tyr Asp Ser Ile Asp
 595 600 605
 Leu Ser Glu Pro Leu Gln Asn Ile His Leu Leu Ser Leu Ser Asp Val
 610 615 620
 50 Thr Ala Arg His Ile Asn Thr Asp Asn Phe His Pro Glu Ser Leu Asn
 625 630 635 640
 Ala Thr Glu His Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Val
 645 650 655
 Glu Thr Ile Thr Thr Asn Asn Ala Ser Ile Glu Thr Ala Asn Thr
 660 665 670
 60 Leu Tyr Arg Ala Leu Tyr Ala Asn Trp Thr Pro Leu Gly Tyr Lys Val
 675 680 685

74/83

	Asn Pro Glu Tyr Gln Gly Asp Leu Ala Thr Thr Pro Leu Trp Gln Ser			
	690	695	700	
	Phe His Thr Met Phe Ser Leu Leu Arg Ser Tyr Asn Arg Thr Gly Asp			
	705	710	715	720
10	Ser Asp Ile Glu Arg Pro Phe Leu Glu Ile Gln Gly Ile Ala Asp Gly			
	725	730	735	
	Leu Phe Val His Gln Asn Ser Ile Pro Gly Ala Pro Gly Phe Arg Ile			
	740	745	750	
	Gln Ser Thr Gly Tyr Ser Leu Gln Ala Ser Ser Glu Thr Ser Leu His			
	755	760	765	
20	Gln Lys Ile Ser Leu Gly Phe Ala Gln Phe Phe Thr Arg Thr Lys Glu			
	770	775	780	
	Ile Gly Ser Ser Asn Asn Val Ser Ala His Asn Thr Val Ser Ser Leu			
	785	790	795	800
	Tyr Val Glu Leu Pro Trp Phe Gln Glu Ala Phe Ala Thr Ser His Ser			
	805	810	815	
	Leu Ala Tyr Gly Tyr Gly Asp His His Leu His Ala Tyr Ile Arg His			
	820	825	830	
30	Ile Lys Asn Arg Ala Glu Gly Thr Cys Tyr Ser His Thr Leu Ala Ala			
	835	840	845	
	Ala Ile Gly Cys Ser Phe Pro Trp Gln Gln Lys Ser Tyr Leu His Leu			
	850	855	860	
	Ser Pro Phe Val Gln Ala Ile Ala Ile Arg Ser His Gln Thr Ala Phe			
	865	870	875	880
40	Glu Glu Ile Gly Asp Asn Pro Arg Lys Phe Val Ser Gln Lys Pro Phe			
	885	890	895	
	Tyr Asn Leu Thr Leu Pro Leu Gly Ile Gln Gly Lys Trp Gln Ser Lys			
	900	905	910	
	Phe His Val Pro Thr Glu Trp Thr Leu Glu Leu Ser Tyr Gln Pro Val			
	915	920	925	
	Leu Tyr Gln Gln Asn Pro Gln Ile Gly Val Thr Leu Leu Ala Ser Gly			
	930	935	940	
50	Gly Ser Trp Asp Ile Leu Gly His Asn Tyr Val Arg Asn Ala Leu Gly			
	945	950	955	960
	Tyr Lys Val His Asn Gln Thr Ala Leu Phe Arg Ser Leu Asp Leu Phe			
	965	970	975	
	Leu Asp Tyr Gln Gly Ser Val Ser Ser Ser Thr Ser Thr His His Leu			
	980	985	990	
60	Gln Ala Gly Ser Thr Leu Lys Phe			
	995	1000		

75/83

<210> 43
<211> 931
<212> PRT
<213> Chlamydia pneumoniae

<400> 43
Met Leu Leu Pro Phe Thr Phe Val Leu Ala Asn Glu Gly Leu Gln Leu
10 1 5 10 15

Pro Leu Glu Thr Tyr Ile Thr Leu Ser Pro Glu Tyr Gln Ala Ala Pro
20 25 30

Gln Val Gly Phe Thr His Asn Gln Asn Gln Asp Leu Ala Ile Val Gly
35 40 45

Asn His Asn Asp Phe Ile Leu Asp Tyr Lys Tyr Tyr Arg Ser Asn Gly
50 55 60

20 Gly Ala Leu Thr Cys Lys Asn Leu Leu Ile Ser Glu Asn Ile Gly Asn
65 70 75 80

Val Phe Phe Glu Lys Asn Val Cys Pro Asn Ser Gly Gly Ala Ile Tyr
85 90 95

Ala Ala Gln Asn Cys Thr Ile Ser Lys Asn Gln Asn Tyr Ala Phe Thr
100 105 110

30 Thr Asn Leu Val Ser Asp Asn Pro Thr Ala Thr Ala Gly Ser Leu Leu
115 120 125

Gly Gly Ala Leu Phe Ala Ile Asn Cys Ser Ile Thr Asn Asn Leu Gly
130 135 140

Gln Gly Thr Phe Val Asp Asn Leu Ala Leu Asn Lys Gly Gly Ala Leu
145 150 155 160

Tyr Thr Glu Thr Asn Leu Ser Ile Lys Asp Asn Lys Gly Pro Ile Ile
40 165 170 175

Ile Lys Gln Asn Arg Ala Leu Asn Ser Asp Ser Leu Gly Gly Ile
180 185 190

Tyr Ser Gly Asn Ser Leu Asn Ile Glu Gly Asn Ser Gly Ala Ile Gln
195 200 205

Ile Thr Ser Asn Ser Ser Gly Ser Gly Gly Ile Phe Ser Thr Gln
210 215 220

50 Thr Leu Thr Ile Ser Ser Asn Lys Lys Leu Ile Glu Ile Ser Glu Asn
225 230 235 240

Ser Ala Phe Ala Asn Asn Tyr Gly Ser Asn Phe Asn Pro Gly Gly Gly
245 250 255

Gly Leu Thr Thr Phe Cys Thr Ile Leu Asn Asn Arg Glu Gly Val
260 265 270

60 Leu Phe Asn Asn Asn Gln Ser Gln Ser Asn Gly Gly Ala Ile His Ala
275 280 285

76/83

Lys Ser Ile Ile Ile Lys Glu Asn Gly Pro Val Tyr Phe Leu Asn Asn
 290 295 300
 Thr Ala Thr Arg Gly Gly Ala Leu Leu Asn Leu Ser Ala Gly Ser Gly
 305 310 315 320
 Asn Gly Ser Phe Ile Leu Ser Ala Asp Asn Gly Asp Ile Ile Phe Asn
 10 325 330 335
 Asn Asn Thr Ala Ser Lys His Ala Leu Asn Pro Pro Tyr Arg Asn Ala
 340 345 350
 Ile His Ser Thr Pro Asn Met Asn Leu Gln Ile Gly Ala Arg Pro Gly
 355 360 365
 Tyr Arg Val Leu Phe Tyr Asp Pro Ile Glu His Glu Leu Pro Ser Ser
 370 375 380
 20 Phe Pro Ile Leu Phe Asn Phe Glu Thr Gly His Thr Gly Thr Val Leu
 385 390 395 400
 Phe Ser Gly Glu His Val His Gln Asn Phe Thr Asp Glu Met Asn Phe
 405 410 415
 Phe Ser Tyr Leu Arg Asn Thr Ser Glu Leu Arg Gln Gly Val Leu Ala
 420 425 430
 30 Val Glu Asp Gly Ala Gly Leu Ala Cys Tyr Lys Phe Phe Gln Arg Gly
 435 440 445
 Gly Thr Leu Leu Leu Gly Gln Gly Ala Val Ile Thr Thr Ala Gly Thr
 450 455 460
 Ile Pro Thr Pro Ser Ser Thr Pro Thr Thr Val Gly Ser Thr Ile Thr
 465 470 475 480
 Leu Asn His Ile Ala Ile Asp Leu Pro Ser Ile Leu Ser Phe Gln Ala
 40 485 490 495
 Gln Ala Pro Lys Ile Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr
 500 505 510
 Thr Glu Asp Ser Asn Pro Thr Ile Thr Ile Ser Gly Thr Leu Thr Leu
 515 520 525
 Arg Asn Ser Asn Asn Glu Asp Pro Tyr Asp Ser Leu Asp Leu Ser His
 530 535 540
 50 Ser Leu Glu Lys Val Pro Leu Leu Tyr Ile Val Asp Val Ala Ala Gln
 545 550 555 560
 Lys Ile Asn Ser Ser Gln Leu Asp Leu Ser Thr Leu Asn Ser Gly Glu
 565 570 575
 His Tyr Gly Tyr Gln Gly Ile Trp Ser Thr Tyr Trp Val Glu Thr Thr
 580 585 590
 60 Thr Ile Thr Asn Pro Thr Ser Leu Leu Gly Ala Asn Thr Lys His Lys
 595 600 605

77/83

	Leu	Leu	Tyr	Ala	Asn	Trp	Ser	Pro	Leu	Gly	Tyr	Arg	Pro	His	Pro	Glu
	610						615					620				
	Arg	Arg	Gly	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Trp	Gln	Ser	Ala	Tyr	Thr
	625					630					635					640
10	Ala	Leu	Ala	Gly	Leu	His	Ser	Leu	Ser	Ser	Trp	Asp	Glu	Glu	Lys	Gly
						645			650						655	
	His	Ala	Ala	Ser	Leu	Gln	Gly	Ile	Gly	Leu	Leu	Val	His	Gln	Lys	Asp
						660			665						670	
	Lys	Asn	Gly	Phe	Lys	Gly	Phe	Arg	Ser	His	Met	Thr	Gly	Tyr	Ser	Ala
							675			680					685	
20	Thr	Thr	Glu	Ala	Thr	Ser	Ser	Gln	Ser	Pro	Asn	Phe	Ser	Leu	Gly	Phe
							690			695					700	
	Ala	Gln	Phe	Phe	Ser	Lys	Ala	Lys	Glu	His	Glu	Ser	Gln	Asn	Ser	Thr
		705				710				715					720	
	Ser	Ser	His	His	Tyr	Phe	Ser	Gly	Met	Cys	Ile	Ala	Lys	Tyr	Ser	Leu
						725				730					735	
	Gln	Arg	Val	Ile	Arg	Leu	Ser	Val	Ser	Leu	Ala	Tyr	Met	Phe	Thr	Ser
						740			745						750	
30	Glu	His	Thr	His	Thr	Met	Tyr	Gln	Gly	Leu	Leu	Glu	Gly	Asn	Ser	Gln
						755			760						765	
	Gly	Ser	Phe	His	Asn	His	Thr	Leu	Ala	Gly	Ala	Leu	Ser	Cys	Val	Phe
							770			775					780	
	Leu	Pro	Gln	Pro	His	Gly	Glu	Ser	Leu	Gln	Ile	Tyr	Pro	Phe	Ile	Thr
							785			790			795		800	
40	Ala	Leu	Ala	Ile	Arg	Gly	Asn	Leu	Ala	Ala	Phe	Gln	Glu	Ser	Gly	Asp
							805			810					815	
	His	Ala	Arg	Glu	Phe	Ser	Leu	His	Arg	Pro	Leu	Thr	Asp	Val	Ser	Leu
							820			825					830	
	Pro	Val	Gly	Ile	Arg	Ala	Ser	Trp	Lys	Asn	His	His	Arg	Val	Pro	Leu
							835			840					845	
	Val	Trp	Leu	Thr	Glu	Ile	Ser	Tyr	Arg	Ser	Thr	Leu	Tyr	Arg	Gln	Asp
							850			855			860			
50	Pro	Glu	Leu	His	Ser	Lys	Leu	Leu	Ile	Ser	Gln	Gly	Thr	Trp	Thr	Thr
							865			870			875		880	
	Gln	Ala	Thr	Pro	Val	Thr	Tyr	Asn	Ala	Leu	Gly	Ile	Lys	Val	Lys	Asn
							885			890					895	
	Thr	Met	Gln	Val	Phe	Pro	Lys	Val	Thr	Leu	Ser	Leu	Asp	Tyr	Ser	Ala
							900			905					910	
60	Asp	Ile	Ser	Ser	Ser	Thr	Leu	Ser	His	Tyr	Leu	Asn	Val	Ala	Ser	Arg
							915			920					925	

78/83

Met Arg Phe
930

<210> 44
<211> 978
<212> PRT
10 <213> Chlamydia pneumoniae

<400> 44
Met Pro Leu Ser Phe Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu
1 5 10 15

Cys Ser Ala Ser Cys Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe
20 25 30

Val Pro Pro Ile Thr Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser Asp
20 35 40 45

Phe Val Cys Ser Asn Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe Ile
50 55 60

Asn Ser Ser Ser Asn Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr
65 70 75 80

Phe Thr Ser Cys Gln Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser
85 90 95

30 Ala Ala Glu Thr Leu Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr
100 105 110

Gly Asn Gln Ser Thr Gly Leu Gly Leu Ile Tyr Gly Lys Asp Ile
115 120 125

Val Phe Gln Ser Ile Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala
130 135 140

40 Tyr Ser Pro Ala Ser Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr
145 150 155 160

Val Thr Thr Gly Ala Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val
165 170 175

Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe
180 185 190

Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn
50 195 200 205

Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly
210 215 220

Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly
225 230 235 240

Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val
245 250 255

79/83

Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys
 260 265 270
 Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr
 275 280 285
 Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu
 10 290 295 300
 Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu Asp Ser Asn
 305 310 315 320
 Thr Ala Ala Arg Asn Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile
 325 330 335
 Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly
 20 340 345 350
 Gly Ala Ile Phe Ile Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr
 355 360 365
 Ser Thr Leu Thr Ile Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly
 370 375 380
 Asn Met Leu Asn Thr Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu
 385 390 395 400
 30 Ala Gly Gly Glu Ile Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu
 405 410 415
 Val Phe Tyr Asp Pro Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser
 420 425 430
 Asn Lys Asp Ile Thr Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val
 435 440 445
 Phe Thr Ser Lys Gly Leu Ser Ser Thr Glu Leu Leu Leu Pro Ala Asn
 40 450 455 460
 Thr Thr Thr Ile Leu Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu
 465 470 475 480
 Lys Ile Thr Asp Asn Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln
 485 490 495
 Gly Ser Gly Gln Leu Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala
 50 500 505 510
 Thr Pro Thr Gly Ala Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu
 515 520 525
 Ala Phe Asp Pro Phe Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser
 530 535 540
 Val Asn Ala Gly Thr Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu
 545 550 555 560
 60 Asp Glu His Asp Val Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser
 565 570 575

80/83

Pro Val Ala Ile Pro Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys
 580 585 590
 Thr Gly Phe Pro Asp Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr
 595 600 605
 Gln Gly Lys Trp Ser Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala
 10 610 615 620
 Pro Asp Gly Gly Phe Pro Gly Pro Ser Pro Ser Ala Asn Thr Leu
 625 630 635 640
 Tyr Ala Val Trp Asn Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu
 645 650 655
 Asp Pro Glu Arg Tyr Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser
 20 660 665 670
 Phe Leu Gly Asn Gln Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu
 675 680 685
 Ile Asp His Pro Gly Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr
 690 695 700
 Val Glu His Thr Pro Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr
 705 710 715 720
 30 Gly Gly Tyr Gln Ala Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr
 725 730 735
 Leu Gly Leu Ser Phe Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro
 740 745 750
 Tyr Asp Ser Arg Cys Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly
 755 760 765
 Gln Phe Pro Ile Val Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys
 40 770 775 780
 Ala Ala Tyr Gly Tyr Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg
 785 790 795 800
 Pro Asp Lys Ala Pro Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr
 805 810 815
 Tyr Val Leu Ile Ser Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu
 820 825 830
 50 Thr Arg Pro Leu Ala Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala
 835 840 845
 Glu Phe Leu Gly Gly Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu
 850 855 860
 Gln Arg Ser Phe Ser Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile
 865 870 875 880
 60 Gly Cys Ser Ser Gln Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr
 885 890 895

Leu Thr Ile Lys Leu Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro
 900 905 910
 His Asn Ile Val Thr Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser
 915 920 925
 Gly Ala Asn Leu Arg Arg His Gly Leu Phe Val Gln Ile His Asp Val
 10 930 935 940
 Val Asp Leu Thr Glu Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp
 945 950 955 960
 Gly Lys Asn Gly Phe Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser
 965 970 975
 Thr Phe
 20
 <210> 45
 <211> 813
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 45
 Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val
 1 5 10
 30 Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe
 15 20 25
 Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn
 30 35 40
 Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly
 45 50 55
 Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly
 40 60 65 70 75
 Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val
 80 85 90
 Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys
 95 100 105
 Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr
 110 115 120
 50 Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu
 125 130 135
 Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn
 140 145 150 155
 Thr Ala Ala Arg Asn Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile
 160 165 170
 60 Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly
 175 180 185

82/83

Gly Ala Ile Phe Ile Gly Pro Ser Val Gly Asp Pro Ala Lys Gln Thr
 190 195 200
 Ser Thr Leu Thr Ile Leu Ala Ser Glu Gly Asp Ile Ala Phe Gln Gly
 205 210 215
 Asn Met Leu Asn Thr Lys Pro Gly Ile Arg Asn Ala Ile Thr Val Glu
 10 220 225 230 235
 Ala Gly Gly Glu Ile Val Ser Leu Ser Ala Gln Gly Gly Ser Arg Leu
 240 245 250
 Val Phe Tyr Asp Pro Ile Thr His Ser Leu Pro Thr Thr Ser Pro Ser
 255 260 265
 Asn Lys Asp Ile Thr Ile Asn Ala Asn Gly Ala Ser Gly Ser Val Val
 270 275 280
 20 Phe Thr Ser Lys Gly Leu Ser Ser Thr Glu Leu Leu Pro Ala Asn
 285 290 295
 Thr Thr Thr Ile Leu Leu Gly Thr Val Lys Ile Ala Ser Gly Glu Leu
 300 305 310 315
 Lys Ile Thr Asp Asn Ala Val Val Asn Val Ala Gly Phe Ala Thr Gln
 320 325 330
 Gly Ser Gly Gln Leu Thr Leu Gly Ser Gly Gly Thr Leu Gly Leu Ala
 30 335 340 345
 Thr Pro Thr Gly Ala Pro Ala Ala Val Asp Phe Thr Ile Gly Lys Leu
 350 355 360
 Ala Phe Asp Pro Phe Ser Phe Leu Lys Arg Asp Phe Val Ser Ala Ser
 365 370 375
 Val Asn Ala Gly Thr Lys Asn Val Thr Leu Thr Gly Ala Leu Val Leu
 40 380 385 390 395
 Asp Glu His Asp Val Thr Asp Leu Tyr Asp Met Val Ser Leu Gln Ser
 400 405 410
 Pro Val Ala Ile Pro Ile Ala Val Phe Lys Gly Ala Thr Val Thr Lys
 445 420 425
 Thr Gly Phe Pro Asp Gly Glu Ile Ala Thr Pro Ser His Tyr Gly Tyr
 430 435 440
 50 Gln Gly Lys Trp Ser Tyr Thr Trp Ser Arg Pro Leu Leu Ile Pro Ala
 445 450 455
 Pro Asp Gly Gly Phe Pro Gly Gly Pro Ser Pro Ser Ala Asn Thr Leu
 460 465 470 475
 Tyr Ala Val Trp Asn Ser Asp Thr Leu Val Arg Ser Thr Tyr Ile Leu
 480 485 490
 Asp Pro Glu Arg Tyr Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser
 60 495 500 505

83/83

Phe Leu Gly Asn Gln Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu
 510 515 520

Ile Asp His Pro Gly Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr
 525 530 535

Val Glu His Thr Pro Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr
 10 540 545 550 555

Gly Gly Tyr Gln Ala Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr
 560 565 570

Leu Gly Leu Ser Phe Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro
 575 580 585

Tyr Asp Ser Arg Cys Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly
 590 595 600

20 Gln Phe Pro Ile Val Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys
 605 610 615

Ala Ala Tyr Gly Tyr Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg
 620 625 630 635

Pro Asp Lys Ala Pro Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr
 640 645 650

30 Tyr Val Leu Ile Ser Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu
 655 660 665

Thr Arg Pro Leu Ala Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala
 670 675 680

Glu Phe Leu Gly Gly Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu
 685 690 695

40 Gln Arg Ser Phe Ser Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile
 700 705 710 715

Gly Cys Ser Ser Gln Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr
 720 725 730

Leu Thr Ile Lys Leu Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro
 735 740 745

His Asn Ile Val Thr Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser
 750 755 760

50 Gly Ala Asn Leu Arg Arg His Gly Leu Phe Val Gln Ile His Asp Val
 765 770 775

Val Asp Leu Thr Glu Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp
 780 785 790 795

Gly Lys Asn Gly Phe Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser
 800 805 810

60 Thr Phe